

Europäisches Patentamt

European Patent Office

Offi uropéen d s brev ts



(11)

EP 1 219 712 A1

(12)

EUROPEAN PATENT APPLICATION

published in accordance with Art. 158(3) EPC

(43) Date of publication:

03.07.2002 Bulletin 2002/27

(21) Application number: 00964654.8

(22) Date of filing: 04.10.2000

(51) Int Cl.7: **C12N 15/60**, C12N 15/54,
C12N 15/53, C12N 15/31,
C12N 15/56, C12N 9/88,
C12N 9/12, C12N 9/04,
C07K 14/34, C12N 9/26,
C12P 13/04

(86) International application number:

PCT/JP00/06913

(87) International publication number:

WO 01/25447 (12.04.2001 Gazette 2001/15)

(84) Designated Contracting States:

AT BE CH CY DE DK ES FI FR GB GR IE IT LI LU
MC NL PT SE

Designated Extension States:

AL LT LV MK RO SI

(30) Priority: 04.10.1999 JP 28271699

01.11.1999 JP 31114799

21.04.2000 JP 2000120687

(71) Applicant: Ajinomoto Co., Inc.

Tokyo 104-8315 (JP)

(72) Inventors:

- HIRANO, Selko Ajinomoto Co. Inc.
Fermentat. & Bio. Lab.
Kawasaki-shi, Kanagawa 210-8681 (JP)
- NONAKA, Gen Ajinomoto Co. Inc.
Fermentation & Bio. Lab.
Kawasaki-shi, Kanagawa 210-8681 (JP)
- MATSUZAKI, Yumi Ajinomoto Co. Inc.
Fermenta. & Bio. Lab
Kawasaki-shi, Kanagawa 210-86 (JP)
- AKIYOSHI, Naoki Ajinomoto Co. Inc.
Fermenta. & Bio. Lab
Kawasaki-shi, Kanagawa 210-86 (JP)

• NAKAMURA, Kanae 902 Stamford Court 8A
Hochiminh City (VN)

• KIMURA, Eiichiro Ajinomoto Co. Inc.

Fermenta. & Bio. Lab

Kawasaki-shi, Kanagawa 210-8 (JP)

• OSUMI, Tsuyoshi Ajinomoto Co. Inc.

Fermenta. & Bio. Lab

Kawasaki-shi, Kanagawa 210-86 (JP)

• MATSUI, Kazuhiko Ajinomoto Co. Inc.

Fermenta. Bio. Lab

Kawasaki-shi, Kanagawa 210-8 (JP)

• KAWAHARA, Yoshio Ajinomoto Co. Inc.

Fermenta. Bio. Lab

Kawasaki-shi, Kanagawa 210-8 (JP)

• KURAHASHI, Osamu Ajinomoto Co. Inc.

Fermenta. Bio. Lab

Kawasaki-shi, Kanagawa 210-8 (JP)

• NAKAMATSU, Tsuyoshi Ajinomoto Co. Inc.

Ferme. Bio. Lab

Kawasaki-shi, Kanagawa 21 (JP)

• SUGIMOTO, Shinichi Ajinomoto Co. Inc.

Fermen. Bio. Lab

Kawasaki-shi, Kanagawa 210 (JP)

(74) Representative: Strehl Schübel-Hopf & Partner

Maximilianstrasse 54

80538 München (DE)

(54) **THERMOPHILIC AMINO ACID BIOSYNTHESIS SYSTEM ENZYME GENE OF
THERMOTOLERANT CORYNEFORM BACTERIUM**

(57) A plurality of primer sets are designed based on a region where conservation at the amino acid level is observed among various microorganisms for known gene sequences corresponding to a gene coding for an enzyme of the L-amino acid biosynthetic pathway derived from *Corynebacterium thermoaminogenes*, preferably an enzyme that functions at a higher temperature compared with that of *Corynebacterium glutamicum*.

PCR is performed by using the primers and chromosomal DNA of *Corynebacterium thermoaminogenes* as a template. The primers with which an amplification fragment has been obtained are used as primers for screening to select a clone containing a target DNA fragment from a plasmid library of chromosomal DNA of *Corynebacterium thermoaminogenes*.

EP 1 219 712 A1

Description

Technical Field

[0001] The present invention relates to heat resistant enzyme genes, in particular, genes for enzymes of biosynthetic pathway and uptake system of L-amino acids such as L-glutamic acid, of *Corynebacterium thermoaminogenes*, which is a thermophilic coryneform bacterium.

Background Art

[0002] The current main stream of the production of L-amino acids such as L-glutamic acid is the fermentative production utilizing coryneform bacteria. As for the fermentative production of L-amino acids, it has been attempted to reduce the cost based on breeding of strains with superior productivity and development of fermentation techniques. Although conventional attempts for realizing the cost reduction were mainly directed to achieving higher yield, energy required for cooling the fermentation heat generated during the culture cannot be ignored in addition to the raw material as the factors concerning the fermentation cost. That is, as for usual microorganisms used for the fermentation, the temperature of the medium rises due to fermentation heat generated by the microorganism themselves during the fermentation, and hence enzymes required for the fermentation may be inactivated or the productive bacteria may be killed. Therefore, it is necessary to cool the medium during the fermentation. Accordingly, in order to reduce the cooling cost, fermentation at high temperatures has been studied for many years. Moreover, if high temperature fermentation becomes possible, the reaction rate may also be improved. However, as for the L-amino acid fermentation, effective high temperature culture has not been realized so far.

[0003] *Corynebacterium thermoaminogenes* is a bacterium classified into coryneform bacteria like *Corynebacterium glutamicum* (*Brevibacterium lactofermentum*), which is commonly used for the fermentation of L-amino acids. However, it shows the optimum growth temperature of 37-43°C, which is higher than that of *Corynebacterium glutamicum*, i.e., 30-35°C, and shows the optimum temperature for L-glutamic acid production of 42-45°C, which is considerably shifted to the high temperature region (Japanese Patent Laid-open (Kokai) No. 63-240779/1988).

[0004] Meanwhile, there have been developed techniques for enhancing L-amino acid producing ability of *Corynebacterium* and *Brevibacterium* bacteria by introducing a gene coding for an L-amino acid synthesis system enzyme derived from *Escherichia coli* or *Corynebacterium glutamicum* into them. Examples of such an enzyme include, for example, citrate synthase (Japanese Patent Publication (Kokoku) No. 7-121228/1995), which is an enzyme of the L-glutamic acid biosynthetic pathway, glutamate dehydrogenase (Japanese Patent Laid-open No. 61-268185/1986), isocitrate dehydrogenase, aconitate hydratase (Japanese Patent Laid-open No. 63-214189) and so forth.

[0005] However, any L-amino acid biosynthesis enzymes and genes coding for them derived from thermophilic coryneform bacteria have not been reported.

Disclosure of the Invention

[0006] An object of the present invention is to provide genes coding for enzymes derived from *Corynebacterium thermoaminogenes*, preferably enzymes that function at a temperature higher than those of *Corynebacterium glutamicum*.

[0007] The inventors of the present invention extensively studied in order to achieve the aforementioned object. As a result, they successfully isolated genes coding for enzymes of the amino acid biosynthetic pathway of *Corynebacterium thermoaminogenes*, or genes coding for proteins involved in the uptake of amino acids into cells, and thus achieved the present invention.

[0008] That is, the present invention provides the followings.

- (1) A protein having the amino acid sequence of SEQ ID NO: 2 or the amino acid sequence of SEQ ID NO: 2 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, which has isocitrate lyase activity and shows 30% or more of residual activity after a heat treatment at 50°C for 5 minutes.
- (2) A protein having the amino acid sequence of SEQ ID NO: 4 or the amino acid sequence of SEQ ID NO: 4 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, which is involved in acyl Co-A carboxylase activity derived from *Corynebacterium thermoaminogenes*.
- (3) A protein having the amino acid sequence of SEQ ID NO: 6 or the amino acid sequence of SEQ ID NO: 6 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, which has DtsR activity derived from *Corynebacterium thermoaminogenes*.
- (4) A protein having the amino acid sequence of SEQ ID NO: 8 or the amino acid sequence of SEQ ID NO: 8 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, which has

DtsR activity derived from *Corynebacterium thermoaminogenes*.

(5) A protein having the amino acid sequence of SEQ ID NO: 10 or the amino acid sequence of SEQ ID NO: 10 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, which shows phosphofructokinase activity at 60°C in an equivalent or higher degree compared with the activity at 30°C.

(6) A protein having the amino acid sequence of SEQ ID NO: 94 or the amino acid sequence of SEQ ID NO: 94 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, which has activity for imparting sucrose assimilating ability to *Corynebacterium thermoaminogenes*.

(7) A protein having any one of the amino acid sequences of SEQ ID NOS: 17-20 or the amino acid sequence of any one of SEQ ID NOS: 17-20 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, which has a function involved in glutamic acid uptake and derived from *Corynebacterium thermoaminogenes*.

(8) A protein having the amino acid sequence of SEQ ID NO: 22 or the amino acid sequence of SEQ ID NO: 22 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, which has pyruvate dehydrogenase activity derived from *Corynebacterium thermoaminogenes*.

(9) A protein having the amino acid sequence of SEQ ID NO: 24 or the amino acid sequence of SEQ ID NO: 24 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, which has pyruvate carboxylase activity derived from *Corynebacterium thermoaminogenes*.

(10) A protein having the amino acid sequence of SEQ ID NO: 26 or the amino acid sequence of SEQ ID NO: 26 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, which has phosphoenolpyruvate carboxylase activity and shows 50% or more of residual activity after a heat treatment at 45°C for 5 minutes.

(11) A protein having the amino acid sequence of SEQ ID NO: 28 or the amino acid sequence of SEQ ID NO: 28 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, which has aconitase activity and shows 30% or more of residual activity after a heat treatment at 50°C for 3 minutes.

(12) A protein having the amino acid sequence of SEQ ID NO: 30 or the amino acid sequence of SEQ ID NO: 30 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, which has isocitrate dehydrogenase activity and shows 50% or more of residual activity after a heat treatment at 45°C for 10 minutes.

(13) A protein having the amino acid sequence of SEQ ID NO: 32 or the amino acid sequence of SEQ ID NO: 32 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, which has dihydrolipoamide dehydrogenase activity derived from *Corynebacterium thermoaminogenes*.

(14) A protein having the amino acid sequence of SEQ ID NO: 34 or the amino acid sequence of SEQ ID NO: 34 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, which has 2-oxoglutarate dehydrogenase activity and shows 30% or more of residual activity after a heat treatment at 50°C for 10 minutes.

(15) A protein having the amino acid sequence of SEQ ID NO: 80 in Sequence Listing or the amino acid sequence of SEQ ID NO: 80 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, which shows glutamate dehydrogenase activity at 42°C in an equivalent or higher degree compared with the activity at 37°C.

(16) A protein having the amino acid sequence of SEQ ID NO: 90 in Sequence Listing or the amino acid sequence of SEQ ID NO: 90 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, which shows citrate synthase activity at 37°C in an equivalent or higher degree compared with the activity at 23°C.

(17) A DNA which codes for a protein having the amino acid sequence of SEQ ID NO: 2 or the amino acid sequence of SEQ ID NO: 2 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, and having isocitrate lyase activity.

(18) The DNA according to (17), which is a DNA defined in the following (a1) or (b1):

(a1) a DNA which comprises the nucleotide sequence of SEQ ID NO: 1 in Sequence Listing,

(b1) a DNA which is hybridizable with the nucleotide sequence of SEQ ID NO: 1 in Sequence Listing or a primer prepared based on the nucleotide sequence under a stringent condition, and codes for a protein having isocitrate lyase activity.

(19) A DNA which codes for a protein having the amino acid sequence of SEQ ID NO: 4 or the amino acid sequence of SEQ ID NO: 4 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, and involved in acyl Co-A carboxylase activity.

(20) The DNA according to (19), which is a DNA defined in the following (a2) or (b2):

- (a2) a DNA which comprises the nucleotide sequence of SEQ ID NO: 3 in Sequence Listing,
 (b2) a DNA which is hybridizable with the nucleotide sequence of SEQ ID NO: 3 in Sequence Listing or a primer prepared based on the nucleotide sequence under a stringent condition, and codes for a protein involved in acyl Co-A carboxylase activity.

(21) A DNA which codes for a protein having the amino acid sequence of SEQ ID NO: 6 or the amino acid sequence of SEQ ID NO: 6 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, and having DtsR activity.

(22) The DNA according to (21), which is a DNA defined in the following (a3) or (b3):

- (a3) a DNA which comprises the nucleotide sequence of SEQ ID NO: 5 in Sequence Listing,
 (b3) a DNA which is hybridizable with the nucleotide sequence of SEQ ID NO: 5 in Sequence Listing or a primer prepared based on the nucleotide sequence under a stringent condition, and codes for a protein having DtsR activity.

(23) A DNA which codes for a protein having the amino acid sequence of SEQ ID NO: 8 or the amino acid sequence of SEQ ID NO: 8 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, and having DtsR activity.

(24) The DNA according to (23), which is a DNA defined in the following (a4) or (b4):

- (a4) a DNA which comprises the nucleotide sequence of SEQ ID NO: 7 in Sequence Listing,
 (b4) a DNA which is hybridizable with the nucleotide sequence of SEQ ID NO: 7 in Sequence Listing or a primer prepared based on the nucleotide sequence under a stringent condition, and codes for a protein having DtsR activity.

(25) A DNA which codes for a protein having the amino acid sequence of SEQ ID NO: 10 or the amino acid sequence of SEQ ID NO: 10 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, and having phosphofructokinase activity.

(26) The DNA according to (25), which is a DNA defined in the following (a5) or (b5):

- (a5) a DNA which comprises the nucleotide sequence of SEQ ID NO: 9 in Sequence Listing,
 (b5) a DNA which is hybridizable with the nucleotide sequence of SEQ ID NO: 9 in Sequence Listing or a primer prepared based on the nucleotide sequence under a stringent condition, and codes for a protein having phosphofructokinase activity.

(27) A DNA which codes for a protein having the amino acid sequence of SEQ ID NO: 93 or the amino acid sequence of SEQ ID NO: 93 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, and having invertase activity.

(28) The DNA according to (27), which is a DNA defined in the following (a6) or (b6):

- (a6) a DNA which comprises the nucleotide sequence of SEQ ID NO: 93 in Sequence Listing,
 (b6) a DNA which is hybridizable with the nucleotide sequence of SEQ ID NO: 93 in Sequence Listing or a primer prepared based on the nucleotide sequence under a stringent condition, and codes for a protein having invertase activity.

(29) A DNA which codes for a protein having any one of the amino acid sequences of SEQ ID NOS: 17-20 or the amino acid sequence of any one of SEQ ID NOS: 17-20 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, and having a function involved in glutamic acid uptake.

(30) The DNA according to (29), which is a DNA defined in the following (a7) or (b7):

- (a7) a DNA which comprises the nucleotide sequence of SEQ ID NO: 16 in Sequence Listing,
 (b7) a DNA which is hybridizable with the nucleotide sequence of SEQ ID NO: 16 in Sequence Listing or a primer prepared based on the nucleotide sequence under a stringent condition, and codes for a protein having a function involved in glutamic acid uptake.

(31) A DNA which codes for a protein having the amino acid sequence of SEQ ID NO: 22 or the amino acid sequence of SEQ ID NO: 22 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, and having pyruvate dehydrogenase activity.

(32) The DNA according to (31), which is a DNA defined in the following (a8) or (b8):

(a8) a DNA which comprises the nucleotide sequence of SEQ ID NO: 21 in Sequence Listing.

(b8) a DNA which is hybridizable with the nucleotide sequence of SEQ ID NO: 21 in Sequence Listing or a primer prepared based on the nucleotide sequence under a stringent condition, and codes for a protein having pyruvate dehydrogenase activity.

(33) A DNA which codes for a protein having the amino acid sequence of SEQ ID NO: 24 or the amino acid sequence of SEQ ID NO: 24 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, and having pyruvate carboxylase activity.

(34) A DNA according to (33), which is a DNA defined in the following (a9) or (b9):

(a9) a DNA which comprises the nucleotide sequence of SEQ ID NO: 23 in Sequence Listing.

(b9) a DNA which is hybridizable with the nucleotide sequence of SEQ ID NO: 23 in Sequence Listing or a primer prepared based on the nucleotide sequence under a stringent condition, and codes for a protein having pyruvate carboxylase activity.

(35) A DNA which codes for a protein having the amino acid sequence of SEQ ID NO: 26 or the amino acid sequence of SEQ ID NO: 26 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, and having phosphoenolpyruvate carboxylase activity.

(36) The DNA according to (35), which is a DNA defined in the following (a10) or (b10):

(a10) a DNA which comprises the nucleotide sequence of SEQ ID NO: 25 in Sequence Listing.

(b10) a DNA which is hybridizable with the nucleotide sequence of SEQ ID NO: 25 in Sequence Listing or a primer prepared based on the nucleotide sequence under a stringent condition, and codes for a protein having phosphoenolpyruvate carboxylase activity.

(37) A DNA which codes for a protein having the amino acid sequence of SEQ ID NO: 28 or the amino acid sequence of SEQ ID NO: 28 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, and having aconitase activity.

(38) The DNA according to (37), which is a DNA defined in the following (a11) or (b11):

(a11) a DNA which comprises the nucleotide sequence of SEQ ID NO: 27 in Sequence Listing.

(b11) a DNA which is hybridizable with the nucleotide sequence of SEQ ID NO: 27 in Sequence Listing or a primer prepared based on the nucleotide sequence under a stringent condition, and codes for a protein having aconitase activity.

(39) A DNA which codes for a protein having the amino acid sequence of SEQ ID NO: 30 or the amino acid sequence of SEQ ID NO: 30 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, and having isocitrate dehydrogenase activity.

(40) The DNA according to (39), which is a DNA defined in the following (a12) or (b12):

(a12) a DNA which comprises the nucleotide sequence of SEQ ID NO: 27 in Sequence Listing.

(b12) a DNA which is hybridizable with the nucleotide sequence of SEQ ID NO: 27 in Sequence Listing or a primer prepared based on the nucleotide sequence under a stringent condition, and codes for a protein having isocitrate dehydrogenase activity.

(41) A DNA which codes for a protein having the amino acid sequence of SEQ ID NO: 32 or the amino acid sequence of SEQ ID NO: 32 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, and having dihydrolipoamide dehydrogenase activity.

(42) The DNA according to (41), which is a DNA defined in the following (a13) or (b13):

(a13) a DNA which comprises the nucleotide sequence of SEQ ID NO: 31 in Sequence Listing.

(b13) a DNA which is hybridizable with the nucleotide sequence of SEQ ID NO: 31 in Sequence Listing or a primer prepared based on the nucleotide sequence under a stringent condition, and codes for a protein having dihydrolipoamide dehydrogenase activity.

(43) A DNA which codes for a protein having the amino acid sequence of SEQ ID NO: 34 or the amino acid

sequence of SEQ ID NO: 34 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, and having 2-oxoglutarate dehydrogenase activity.

(44) The DNA according to (43), which is a DNA defined in the following (a14) or (b14):

(a14) a DNA which comprises the nucleotide sequence of SEQ ID NO: 33 in Sequence Listing.

(b14) a DNA which is hybridizable with the nucleotide sequence of SEQ ID NO: 33 in Sequence Listing or a primer prepared based on the nucleotide sequence under a stringent condition, and codes for a protein having 2-oxoglutarate dehydrogenase activity.

(45) A DNA which codes for a protein having the amino acid sequence of SEQ ID NO: 80 in Sequence Listing or the amino acid sequence of SEQ ID NO: 80 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, and showing glutamate dehydrogenase activity at 42°C in an equivalent or higher degree compared with the activity at 37°C.

(46) The DNA according to (45), which is a DNA defined in the following (a15) or (b15):

(a15) a DNA which comprises the nucleotide sequence of SEQ ID NO: 79 in Sequence Listing.

(b15) a DNA which is hybridizable with the nucleotide sequence of SEQ ID NO: 79 in Sequence Listing or a primer prepared based on the nucleotide sequence under a stringent condition, and codes for a protein showing glutamate dehydrogenase activity at 42°C in an equivalent or higher degree compared with the activity at 37°C.

(47) A DNA which codes for a protein having the amino acid sequence of SEQ ID NO: 90 in Sequence Listing or the amino acid sequence of SEQ ID NO: 90 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, and showing citrate synthase activity at 37°C in an equivalent or higher degree compared with the activity at 23°C.

(48) The DNA according to (47), which is a DNA defined in the following (a16) or (b16):

(a16) a DNA which comprises the nucleotide sequence of SEQ ID NO: 89 in Sequence Listing.

(b16) a DNA which is hybridizable with the nucleotide sequence of SEQ ID NO: 89 in Sequence Listing or a primer prepared based on the nucleotide sequence under a stringent condition, and codes for a protein showing citrate synthase activity at 37°C in an equivalent or higher degree compared with the activity at 23°C.

(49) A method for producing L-amino acid, which comprises culturing a microorganism introduced with a DNA according to any one of (17) to (48) in a medium to produce and accumulate L-amino acid in the medium, and collecting the L-amino acid from the medium.

[0009] The term "DNA of the present invention" is used hereinafter for referring to either one or all of the aforementioned DNAs.

[0010] Hereafter, the present invention will be explained in detail.

[0011] The nucleotide sequences of the DNA of the present invention, names of the genes, and the proteins encoded by the DNA of the present invention are shown in Table 1.

Table 1

| Nucleotide sequence | Name of gene | Encoded protein (abbreviation) |
|-------------------------------|----------------|----------------------------------|
| SEQ ID NO: 1 | <i>aceA</i> | Isocitrate lyase (ICL) |
| SEQ ID NO: 3 | <i>accBC</i> | acyl Co-A carboxylase BC subunit |
| SEQ ID NO: 5 | <i>dtsR1</i> | DTSR1 protein |
| SEQ ID NO: 7 | <i>dtsR2</i> | DTSR2 protein |
| SEQ ID NO: 9 | <i>pfk</i> | Phosphofructokinase |
| SEQ ID NOS: 11, 13, 15, 93 | <i>scrB</i> | Invertase |
| SEQ ID NO: 16 | <i>gluABCD</i> | glutamic acid uptake system |
| SEQ ID NO: 21 | <i>pdhA</i> | pyruvate dehydrogenase |
| SEQ ID NO: 23 | <i>pc</i> | pyruvate carboxylase |
| SEQ ID NO: 25 | <i>ppc</i> | phosphoenolpyruvate carboxylase |
| SEQ ID NO: 27 | <i>acn</i> | aconitase |

Table 1 (continued)

| Nucleotide sequence | Name of gene | Encoded protein (abbreviation) |
|---------------------|--------------|--------------------------------|
| SEQ ID NO: 29 | <i>icd</i> | isocitrate dehydrogenase |
| SEQ ID NO: 31 | <i>lpd</i> | dihydrolipoamide dehydrogenase |
| SEQ ID NO: 33 | <i>odhA</i> | 2-oxoglutarate dehydrogenase |
| SEQ ID NO: 79 | <i>gdh</i> | glutamate dehydrogenase |
| SEQ ID NO: 89 | <i>gluA</i> | citrate synthase |

[0012] The open reading frames (ORFs) of SEQ ID NOS: 3, 23, 25, 31 and 33 and the fourth ORF of SEQ ID NO: 16 all start from GTG. Although the amino acids encoded by these GTG are indicated as valine in Sequence Listing, they may be methionine.

[0013] The sequence of SEQ ID NO: 16 contains four ORFs, which correspond to *gluA*, *gluB*, *gluC* and *gluD* in this order from the 5' end side.

[0014] The aforementioned DNA sequences were isolated from chromosomal DNA of the *Corynebacterium thermoaminogenes* AJ12310 strain (FERM BP-1542). However, the DNA sequences shown in SEQ ID NOS: 11 and 13 were isolated from *Corynebacterium thermoaminogenes* AJ12340 strain (FERM BP-1539) and AJ12309 strain (FERM BP-1541), respectively, which had invertase activity and sucrose assimilating property, because the AJ12310 strain did not have invertase activity and sucrose assimilating property, and the *scrB* gene isolated from the strain had not any open reading frame.

[0015] The *Corynebacterium thermoaminogenes* AJ12310 strain (also referred to as YS-314 strain) and AJ12309 strain (also referred to as YS-155 strain) were deposited at the National Institute of Bioscience and Human-Technology, Agency of Industrial Science and Technology, Ministry of International Trade and Industry (postal code: 305-8566, 1-3, Higashi 1-chome, Tsukuba-shi, Ibaraki-ken, Japan) on March 13, 1987 and given deposition numbers of FERM P-9246 and FERM P-9245, respectively. Then, they were transferred to international depositions under the provisions of the Budapest Treaty on October 27, 1987, and given deposition numbers of FERM BP-1542 and FERM BP-1541, respectively.

[0016] The AJ12340 strain (also referred to as YS-40 strain) was deposited at the National Institute of Bioscience and Human-Technology, Agency of Industrial Science and Technology, Ministry of International Trade and Industry (postal code: 305-8566, 1-3, Higashi 1-chome, Tsukuba-shi, Ibaraki-ken, Japan) on March 10, 1987 and given a deposition number of FERM P-9277. Then, it was transferred to an international deposition under the provisions of the Budapest Treaty on October 27, 1987, and given a deposition number of FERM BP-1539.

[0017] The nucleotide sequences shown in SEQ ID NOS: 11, 13 and 15 are partial sequences of *scrB*, and the sequences of SEQ ID NOS: 11 and 13 code for partial amino acid sequences of invertase shown in SEQ ID NOS: 12 and 14.

[0018] A DNA sequence containing a partial fragment of a target gene can be obtained by comparing already reported nucleotide sequences for the target gene of various microorganisms such as *Brevibacterium lactofermentum* to select a region containing a well-conserved nucleotide sequence, and carrying out PCR using primers designed based on the nucleotide sequence of the region and chromosomal DNA of *Corynebacterium thermoaminogenes* as a template. Further, by performing hybridization using the obtained DNA fragment or a probe prepared based on the sequence of the fragment to screen a chromosomal DNA library of *Corynebacterium thermoaminogenes*, a DNA fragment containing the gene in its full length can be obtained. A DNA fragment containing the gene in its full length can also be obtained by performing genome walking using the obtained partial fragment of the gene. The genome walking can be carried out by using a commercially available kit, for example, TaKaRa LA PCR in vitro Cloning Kit (produced by Takara Shuzo).

[0019] For example, a partial sequence of DNA coding for glutamate dehydrogenase (henceforth the DNA is also referred to as "*gdh*", and the enzyme is also referred to as "GDH") can be obtained from chromosomal DNA of *Corynebacterium thermoaminogenes* such as the *Corynebacterium thermoaminogenes* AJ12310 strain by PCR (polymerase chain reaction) using the chromosomal DNA as a template and primers having the nucleotide sequences shown in SEQ ID NOS: 77 and 78 of Sequence Listing. Further, by performing genome walking using the obtained partial fragment, the whole *gdh* gene can be obtained.

[0020] Further, a partial sequence of DNA coding for citrate synthase (henceforth the DNA is also referred to as "*gluA*", and the enzyme is also referred to as "CS") can be obtained from chromosomal DNA of *Corynebacterium thermoaminogenes* such as the *Corynebacterium thermoaminogenes* AJ12310 strain by PCR (polymerase chain reaction) using the chromosomal DNA as a template and primers having the nucleotide sequences shown in SEQ ID NOS: 83 and 84 of Sequence Listing. Further, by performing genome walking using the obtained partial fragment, the whole *gluA* gene can be obtained.

[0021] The nucleotide sequences of the aforementioned primers were designed based on a nucleotide sequence in

a region containing a well-conserved nucleotide sequence among the already reported *gdh* genes or *gltA* genes of various microorganisms, which region was found by comparison of the genes:

[0022] As for DNA sequences coding for the other enzymes, partial fragments coding for those enzymes can be similarly obtained by using the primers mentioned in Table 1, and the genes in full length can be obtained by using the

[0023] While the DNA of the present invention was obtained as described above, it can also be obtained from a chromosomal DNA library of *Corynebacterium thermoaminogenes* by hybridization using an oligonucleotide prepared based on the nucleotide sequences of the DNA of the present invention as a probe.

[0024] Methods for preparation of chromosomal DNA, construction of chromosomal DNA library, hybridization, PCR, preparation of plasmid DNA, digestion and ligation of DNA, transformation and so forth are described in Sambrook, J., Fritsch, E.F., Maniatis, T., Molecular Cloning, Cold Spring Harbor Laboratory Press, 1.21 (1989). Further, genome walking can be performed by using a commercially available kit, for example, TaKaRa LA PCR in vitro Cloning Kit (produced by Takara Shuzo).

[0025] Specific methods for obtaining the DNA of the present invention will be explained hereafter.

[0026] First, chromosomal DNA of *Corynebacterium thermoaminogenes* is digested with a suitable restriction enzyme, for example, *Sau3AI*, and fractionated by agarose gel electrophoresis to obtain a DNA fragment of about 4 to 6 kb. The obtained DNA fragment is inserted into a cloning vector such as pHS399, and *Escherichia coli* is transformed with the obtained recombinant plasmid to produce a plasmid library of the chromosomal DNA.

[0027] Separately, primers are produced for use in selecting a clone containing a target gene from a plasmid library by PCR. These primers are designed based on conserved amino acid regions from various microorganisms corresponding to the gene of interest. In the design of primers, a plurality of primer sets are designed considering the codon usage of coryneform bacteria.

[0028] Then, in order to investigate propriety of the produced primers, PCR is performed by using these primers and chromosomal DNA of *Corynebacterium thermoaminogenes* as a template. Further, PCR is performed by using primers from which an amplification fragment has been obtained as primers for screening and a recombinant plasmid prepared from the plasmid library as a template to select a clone containing the target DNA fragment. This operation can be quickly carried out by performing the PCR for every batch including several tens of transformant strains as primary screening and performing colony PCR for the batch with which an amplification fragment was obtained as secondary screening. The fragment lengths of the amplified genes are shown in Tables 2 to 7.

[0029] If a transformant selected as described above contains a target gene is confirmed by preparing a recombinant DNA from the transformant selected as described above, determining the nucleotide sequence of the inserted fragment by the dideoxy termination method, and comparing the nucleotide sequence with a known gene sequence.

[0030] When the obtained DNA fragment contains a part of the target gene, the deleted part is obtained by genome walking.

[0031] The DNA of the present invention may code for a protein including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, so long as the encoded protein has its original function. The number meant by the term "several" may vary depending on positions in the three-dimensional structure of protein or kinds of amino acid residues. However, in general, such a protein preferably shows homology of 30 to 40% or more, more preferably 55 to 65% or more, with respect to a corresponding whole amino acid sequence of the protein. More specifically, the term "several" means a number of 2 to several hundreds, preferably 2 to several tens, more preferably 2 to 10.

[0032] Nucleotide and amino acid sequence were analyzed by, for example, the method developed by Lipman and Pearson (Science, 227, 1435-1441, 1985) by using commercially available software such as Genetyx-Mac computer program (Software Development Co., Tokyo, Japan).

[0033] GDH may be one showing homology of 40 to 80% or more, preferably 80 to 90% or more, for the total amino acid sequence constituting GDH, and showing GDH activity at 42°C equivalent to or higher than the activity at 37°C. In this case, the term "several" means a number of 2 to 30, preferably 2 to 50, more preferably 2 to 10.

[0034] CS may be one showing homology of 40 to 80% or more, preferably 80 to 90% or more, for the total amino acid sequence constituting CS, and showing CS activity at 37°C equivalent to or higher than the activity at 23°C. In this case, the term "several" means a number of 2 to 300, preferably 2 to 50, more preferably 2 to 10.

[0035] A DNA, which codes for the substantially same protein as the original protein as described above, can be obtained by, for example, modifying the nucleotide sequence, for example, by means of the site-directed mutagenesis so that one or more amino acid residues at a specific site should involve substitution, deletion, insertion, addition or inversion. A DNA modified as described above may also be obtained by a conventionally known mutation treatment. The mutation treatment includes a method for treating DNA coding for a target gene in vitro, for example, with hydroxylamine, and a method for treating a microorganism, for example, a bacterium belonging to the genus *Escherichia*, harboring DNA coding for the target gene with ultraviolet irradiation or a mutating agent usually used for the mutation treatment such as N-methyl-N'-nitro-N-nitrosoguanidine (NTG) and nitrous acid.

[0036] The substitution, deletion, insertion, addition, or inversion of nucleotides as described above also includes mutant or variant that naturally occurs due to the difference of strains of *Corynebacterium thermoaminogenes* or the like.

[0037] A DNA coding for substantially the same protein as the original protein can be obtained by expressing DNA having a mutation in an appropriate cell, and investigating activity or function of the expressed product protein. The DNA coding for substantially the same protein as the original protein can also be obtained by, for example, isolating a DNA which is hybridizable with a DNA having each of the nucleotide sequences of the sequences of which sequence numbers are mentioned in Table 1 or a coding region thereof, or a probe designed based on the nucleotide sequence under a stringent condition, and which codes for a protein having the activity originally possessed by the protein, from DNA coding for a protein having a mutation or from a cell harboring it. The activity preferably means each enzymatic activity at 42°C for GDH or 37°C for CS.

[0038] The aforementioned probe can be prepared from a DNA having any one of the nucleotide sequences of which sequence numbers are shown in Table 1 or a DNA having any one of the nucleotide sequences by PCR using suitable primers.

[0039] The "stringent condition" referred to herein is a condition under which so-called specific hybrid is formed, and non-specific hybrid is not formed. It is difficult to clearly express this condition by using any numerical value. However, for example, the stringent condition includes a condition under which DNAs having high homology, for example, DNAs having homology of not less than 50% are hybridized with each other, and DNAs having homology lower than the above are not hybridized with each other. Alternatively, the stringent condition is exemplified by a condition under which DNAs are hybridized with each other at a salt concentration corresponding to an ordinary condition of washing in Southern hybridization, i.e., 60°C, 1 x SSC, 0.1% SDS, preferably 0.1 x SSC, 0.1% SDS.

[0040] The gene, which is hybridizable under the condition as described above, includes those having a stop codon generated in the gene, and those having no activity due to mutation of active site. However, such genes can be easily removed by ligating the genes with a commercially available activity expression vector, and measuring the activity or function.

[0041] A protein corresponding to each DNA of the present invention can be produced by expressing the DNA in a suitable host-vector system.

[0042] As the host used for the expression of a gene, there can be mentioned various prokaryotic cells including *Brevibacterium lactofermentum* (*Corynebacterium glutamicum*), coryneform bacteria such as *Corynebacterium thermoaminogenes*, *Escherichia coli*, *Bacillus subtilis* and so forth, and various eucaryotic cells including *Saccharomyces cerevisiae*, animal cells and plant cells. Among these, prokaryotic cells, in particular, coryneform bacteria and *Escherichia coli* are preferred.

[0043] If the DNA of the present invention is ligated to a vector DNA autonomously replicable in cells of *Escherichia coli* and/or coryneform bacteria and so forth to form a recombinant DNA, and this recombinant DNA is introduced into an *Escherichia coli* cell, the subsequent procedure becomes easy. The vector autonomously replicable in *Escherichia coli* cells is preferably a plasmid vector autonomously replicable in the host cell, and examples thereof include pUC19, pUC18, pBR322, pHSG299, pHSG399, pHSG398, RSF1010 and so forth.

[0044] As the vector autonomously replicable in coryneform bacterium cells, there can be mentioned pAM330 (refer to Japanese Patent Laid-open No. 58-67699/1983), pHM1519 (refer to Japanese Patent Laid-open No. 58-77895/1983) and so forth. Moreover, if a DNA fragment having an ability to make a plasmid autonomously replicable in coryneform bacteria is taken out from these vectors and inserted into the aforementioned vectors for *Escherichia coli*, they can be used as a so-called shuttle vector autonomously replicable in both of *Escherichia coli* and coryneform bacteria.

[0045] Examples of such a shuttle vector include those mentioned below. There are also indicated microorganisms that harbor each vector, and accession numbers thereof at international depositories are shown in the parentheses, respectively.

| | |
|---------|--|
| pAJ655 | <i>Escherichia coli</i> AJ11882 (FERM BP-136) |
| | <i>Corynebacterium glutamicum</i> SR8201 (ATCC39135) |
| pAJ1844 | <i>Escherichia coli</i> AJ11883 (FERM BP-137) |
| | <i>Corynebacterium glutamicum</i> SR8202 (ATCC39136) |
| pAJ611 | <i>Escherichia coli</i> AJ11884 (FERM BP-138) |
| pAJ3148 | <i>Corynebacterium glutamicum</i> SR8203 (ATCC39137) |
| pAJ440 | <i>Bacillus subtilis</i> AJ11901 (FERM BP-140) |
| pHC4 | <i>Escherichia coli</i> AJ12617 (FERM BP-3532) |

[0046] In order to prepare a recombinant DNA by ligating the DNA of the present invention and a vector that functions in coryneform bacteria, the vector is digested with a restriction enzyme that provides an end corresponding to an end of the DNA of the present invention. The ligation is normally attained by using a ligase such as T4 DNA ligase.

[0047] To introduce the recombinant DNA prepared as described above into a host such as coryneform bacteria,

any known transformation methods that have hitherto been reported can be employed. For instance, employable are a method of treating recipient cells with calcium chloride so as to increase the permeability for DNA, which has been reported for *Escherichia coli* K-12 (Mandel, M. and Higa, A., *J. Mol. Biol.*, 53, 159 (1970)), and a method of preparing competent cells from cells which are at the growth phase followed by introducing the DNA thereto, which has been reported for *Bacillus subtilis* (Duncan, C.H., Wilson, G.A. and Young, F.E., *Gene*, 1, 153 (1977)). In addition to these, also employable is a method of making DNA-recipient cells into protoplasts or spheroplasts, which can easily take up recombinant DNA, followed by introducing the recombinant DNA into the cells, which is known to be applicable to *Bacillus subtilis*, actinomycetes and yeasts (Chang, S. and Choen, S.N., *Molec. Gen. Genet.*, 168, 111 (1979); Bibb, M.J., Ward, J.M. and Hopwood, O.A., *Nature*, 274, 398 (1978); Hinnen, A., Hicks, J.B. and Fink, G.R., *Proc. Natl. Sci. USA*, 75, 1929 (1978)). The transformation of coryneform bacteria can be effectively performed by the electric pulse method (refer to Japanese Patent Laid-open No. 2-207791).

[0048] As for the transformation of thermophilic coryneform bacteria such as *Corynebacterium thermoaminogenes*, it can be efficiently performed by treating cells with an agent that changes the structure of cell walls of the host cells, and applying an electric pulse to a solution containing DNA and the cells of which structure of the cell walls have been changed. The aforementioned agent is an agent that can change the structure of cell walls so that the cells can uptake the DNA when an electric pulse is applied to a solution containing the cells treated with the agent and the DNA (henceforth also referred to as a "cell wall treatment agent"). Examples of such an agent include agents that inhibit normal synthesis of bacterial cell wall and agents that lyse bacterial cell walls. Specific examples thereof include lysozyme, penicillin G, glycine and so forth.

[0049] Those cell wall treatment agents may be used each alone, or two or more kinds of them may be used in combination. Among the aforementioned agents, lysozyme and penicillin G are preferred, and lysozyme is particularly preferred.

[0050] Furthermore, the transformation of *Corynebacterium thermoaminogenes* can also be performed by applying an electric pulse to a solution containing DNA and the host cells of which cell walls has been weakened by a physical method such as ultrasonication (*FEMS Microbiology Letters*, 151, 135-138 (1987)).

[0051] In order to efficiently express a gene contained in the DNA of the present invention, a promoter that functions in the host cell such as lac, trp and P_L may be ligated upstream from the coding region of the gene. If a vector containing a promoter is used as the vector, ligation of each gene, vector and promoter can be attained by one step.

[0052] The proteins of the present invention, which can be produced as described above, can be purified as required from a cell extract or medium by using usual methods for purifying enzymes such as ion exchange chromatography, gel filtration chromatography, adsorption chromatography, salting out and solvent precipitation.

[0053] It is expected that the proteins of the present invention are excellent in thermal stability or exhibit higher activity at high temperatures compared with the corresponding proteins of *Corynebacterium glutamicum* and so forth. For example, GDH of *Brevibacterium lactofermentum* shows the highest GDH specific activity around 37°C, and the activity is markedly reduced around 42°C. However, GDH of the present invention shows at 42°C the GDH activity equivalent to or higher than the activity at 37°C. In a preferred embodiment, GDH of the present invention shows the highest specific activity around 42°C, and shows the activity even at 45°C.

[0054] The GDH activity can be measured by, for example, adding the enzyme to 100 mM Tris-HCl (pH 8.0), 20 mM NH_4Cl , 10 mM sodium α -ketoglutarate, 0.25 mM NADPH, and determining change of absorbance at 340 nm (*Molecular Microbiology* 6, 317-326 (1992)).

[0055] Further, CS of *Brevibacterium lactofermentum* shows the highest CS specific activity around 23°C, and the activity is markedly reduced around 33°C. To the contrary, CS of the present invention shows at 37°C the CS activity equivalent to or higher than the activity at 23°C. In a preferred embodiment, CS of the present invention shows reaction temperature-dependently higher activity up to around 37°C, and shows, even at 40°C, about 40% of the activity with respect to the activity at 37°C.

[0056] The CS activity can be measured by, for example, the method described in *Methods in Enzymol.*, 13, 3-11 (1969).

[0057] Further, other proteins of the present invention typically have the following characteristics. The isocitrate lyase has 30% or more of residual activity after a heat treatment at 50°C for 5 minutes. The phosphofructokinase has, at 60°C, the activity equivalent to or higher than the activity at 30°C. The phosphoenolpyruvate carboxylase has 50% or more of residual activity after a heat treatment at 45°C for 5 minutes. The aconitase has 30% or more of residual activity after a heat treatment at 50°C for 3 minutes. The isocitrate dehydrogenase has 50% or more of residual activity after a heat treatment at 45°C for 10 minutes. The 2-oxoglutarate dehydrogenase has 30% or more of residual activity after a heat treatment at 50°C for 10 minutes.

[0058] The proteins of the present invention can also be obtained from cell extracts of *Corynebacterium thermoaminogenes* such as the *Corynebacterium thermoaminogenes* AJ12310 strain by using each activity as an index and usual purification methods for purifying enzymes such as ion exchange chromatography, gel filtration chromatography, adsorption chromatography, salting out and solvent precipitation.

[0059] Among the DNA of the present invention, *pfk*, *pdhA*, *pc*, *ppc*, *acn*, *icd*, *gdh* and *gluA* (names of the enzymes encoded by these are shown in Table 1) can be introduced into L-amino acid production bacteria such as coryneform bacteria to enhance their L-amino acid producing ability. It is also expected that coryneform bacteria introduced with the DNA of the present invention become possible to produce L-amino acid at a temperature higher than usual. The L-amino acid includes L-glutamic acid, L-aspartic acid, L-lysine, L-arginine, L-proline, L-glutamine and so forth.

[0060] For example, it is expected that L-glutamic acid production bacteria such as coryneform bacteria introduced with the *gdh* gene or *gluA* gene come to be able to produce L-glutamic acid at a temperature higher than usual. Further, although CS of *Brevibacterium lactofermentum* may not fully function at a usual culture temperature, for example, 31.5°C, the activity can be enhanced by introducing the *gluA* gene of the present invention.

[0061] Further, *dtsR1* and *dtsR2* are genes that code for proteins imparting resistance to surfactant to coryneform bacteria (DTSR protein), and coryneform L-glutamic acid producing bacteria of which these genes are disrupted produce a marked amount of L-glutamic acid even under a condition where biotin is present in such an amount that a wild strain becomes to be substantially unable to produce L-glutamic acid. Further, if *dtsR1* and *dtsR2* genes of coryneform L-glutamic acid producing bacteria having L-lysine producing ability are amplified, the bacteria are imparted with an ability to produce a marked amount of L-lysine (WO95/23224, Japanese Patent Laid-open (Kokai) No. 10-234371/1998).

[0062] The *scrB* gene can be used for improvement of coryneform bacteria for use in the production of L-amino acids by using coryneform bacteria in a medium containing sucrose.

[0063] By deleting *aceA*, *accBC*, *lpd* or *odhA* of L-glutamic acid producing coryneform bacteria and so forth, their L-glutamic acid productivity can be enhanced. Further, *gluABCD* is a gene cluster of the L-glutamic acid uptake system, and by deleting one to four of *gluA*, *gluB*, *gluC* and *gluD* in coryneform L-glutamic acid producing bacteria, the amount of L-glutamic acid accumulated in the medium can be increased. *aceA*, *accBC*, *lpd*, *odhA* and *gluABCD* of the present invention can be used for disruption of these genes on chromosome.

[0064] The medium used for producing L-amino acids by utilizing a microorganism introduced with the DNA of the present invention may be a usual medium that contains a carbon source, a nitrogen source, inorganic ions and other organic trace nutrients as required. As the carbon source, there can be used hydrocarbons such as glucose, lactose, galactose, fructose, sucrose, blackstrap molasses and starch hydrolysate; alcohols such as ethanol and inositol; or organic acids such as acetic acid, fumaric acid, citric acid and succinic acid.

[0065] As the nitrogen source, there can be used inorganic ammonium salts such as ammonium sulfate, ammonium nitrate, ammonium chloride, ammonium phosphate and ammonium acetate, ammonia, organic nitrogen such as peptone, meat extract, yeast extract, corn steep liquor and soybean hydrolysate, ammonia gas, aqueous ammonia and so forth.

[0066] As the inorganic ions (or sources thereof), added is a small amount of potassium phosphate, magnesium sulfate, iron ions, manganese ions and so forth. As for the organic trace nutrients, it is desirable to add required substances such as vitamin B₁, yeast extract and so forth in a suitable amount as required.

[0067] The culture is preferably performed under an aerobic condition attained by shaking, stirring for aeration or the like for 16 to 72 hours. The culture temperature is controlled to be at 30°C to 47°C, and pH is controlled to be 5 to 9 during the culture. As for the culture temperature, the culture may be performed at a temperature suitable for culture of a microorganism not introduced with the DNA of the present invention or a temperature higher than that. For adjustment of pH, inorganic or organic acidic or alkaline substances, ammonia gas and so forth can be used.

[0068] Collection of L-amino acids from fermentation broth can be attained by a combination of known methods such as techniques utilizing ion exchange resin, precipitation, crystallization and so forth depending on the kind of the L-amino acids.

Brief Explanation of the Drawings

[0069] Fig. 1 shows variation with temperature in activity of glutamate dehydrogenases derived from the *Corynebacterium thermoaminogenes* AJ12310 strain and the *Brevibacterium lactofermentum* 2256 strain.

[0070] Fig. 2 shows thermal stability of glutamate dehydrogenases derived from the AJ12310 strain and the 2256 strain.

[0071] Fig. 3 shows variation with temperature in activity of citrate synthases derived from the AJ12310 strain and the 2256 strain.

[0072] Fig. 4 shows thermal stability of citrate synthases derived from the AJ12310 strain and the 2256 strain.

[0073] Fig. 5 shows variation with temperature in activity of isocitrate lyases derived from the AJ12310 strain and the 2256 strain.

[0074] Fig. 6 shows thermal stability of isocitrate lyases derived from the AJ12310 strain and the 2256 strain.

[0075] Fig. 7 shows variation with temperature in activity of phosphofructokinases derived from the AJ12310 strain and the 2256 strain.

- [0076] Fig. 8 shows thermal stability of phosphofructokinases derived from the AJ12310 strain and the 2256 strain.
- [0077] Fig. 9 shows variation with temperature in activity of phosphoenolpyruvate carboxylases derived from the AJ12310 strain and the 2256 strain.
- [0078] Fig. 10 shows thermal stability of phosphoenolpyruvate carboxylases derived from the AJ12310 strain and the 2256 strain.
- [0079] Fig. 11 shows variation with temperature in activity of aconitases derived from the AJ12310 strain and the 2256 strain.
- [0080] Fig. 12 shows thermal stability of aconitases derived from the AJ12310 strain and the 2256 strain.
- [0081] Fig. 13 shows variation with temperature in activity of isocitrate dehydrogenases derived from the AJ12310 strain and the 2256 strain.
- [0082] Fig. 14 shows thermal stability of isocitrate dehydrogenases derived from the AJ12310 strain and the 2256 strain.
- [0083] Fig. 15 shows thermal stability of 2-oxoglutarate dehydrogenases derived from the AJ12310 strain and the 2256 strain.
- [0084] Fig. 16 shows construction of plasmid pSCR155 carrying *scrB* gene.
- [0085] Fig. 17 shows construction of plasmid pPDHA-2 carrying *pdhA* gene.
- [0086] Fig. 18 shows L-glutamic acid productivity of a *pdhA* gene-amplified strain: (a) 37°C and (b) 44°C.
- [0087] Fig. 19 shows construction of a plasmid pICD-4 carrying *icd* gene.
- [0088] Fig. 20 shows L-glutamic acid productivity of an *icd* gene-amplified strain: (a) 37°C and (b) 44°C.
- [0089] Fig. 21 shows construction of plasmids pHSG299YGDH and pYGDH.
- [0090] Fig. 22 shows construction of plasmids pHSG299YCS and pYCS.

Best Mode for Carrying out the Invention

[0091] Hereafter, the present invention will be further specifically explained with reference to the following examples.

Example 1

<1> Production of plasmid library of *Corynebacterium thermoaminogenes*

[0092] The *Corynebacterium thermoaminogenes* AJ12310 strain was cultured in CM2B liquid medium (1 g/dl of yeast extract (produced by Difco), 1 g/dl of polypeptone (produced by Nippon Seiyaku), 0.5 g/dl of NaCl, 10 µg/dl of biotin, pH 7.0 (adjusted with KOH)) at 37°C for 15 hours, and its chromosomal DNA was prepared from the 10 ml of the medium by using a chromosomal DNA extraction kit (Bacterial Genome DNA Purification Kit (produced by Advanced Genetic Technologies)). The obtained DNA was partially digested with a restriction enzyme *Sau3A*I, and subjected to 0.8% agarose gel electrophoresis to fractionate the DNA. Then, a band corresponding to a DNA fragment of about 4 to 6 kb was excised from the gel, and a DNA fragment of the objective size was obtained by using a DNA gel extraction kit (GIBCO BRL, Concert™ Rapid Gel Extraction System).

[0093] The plasmid pHSG399 (produced by Takara Shuzo) was fully digested with *Bam*HI, and its end was dephosphorylated by using alkaline phosphatase (CIAP; produced by Takara Shuzo). This vector fragment and the aforementioned chromosomal DNA fragment were ligated by using a DNA ligation kit produced by Takara Shuzo, and *Escherichia coli* JM109 was transformed with the obtained recombinant vector. Selection of transformants was performed on LB agar medium (containing 1.5 g/dl of agar) containing 30 µg/ml of chloramphenicol, 0.04 mg/ml of IPTG (isopropyl-β-D-thiogalactopyranoside) and 0.04 mg/ml of X-Gal (5-bromo-4-chloro-3-indolyl-β-D-galactoside) to obtain about 4000 white colonies.

<2> Design of primers for amplification of each gene

[0094] Primers for use in selection of a clone containing each target gene by PCR from the plasmid library obtained above were designed. The target genes were mentioned above.

[0095] The primers were designed based on a known gene sequence of coryneform bacteria, i.e., its sequence of a region where conservation at the amino acid level was observed when compared with corresponding genes of other microorganisms. Considering the codon usage of coryneform bacteria, a plurality of primer sets were designed for each gene.

[0096] To examine propriety of the prepared primers, PCR was performed by using these primers and chromosomal DNA of the *Corynebacterium thermoaminogenes* AJ12310 strain as a template to amplify each gene fragment. As a result, when the PCR was performed by using the primers shown in the upper rows of Tables 2 to 7 under the conditions indicated as "PCR conditions for obtaining partial fragment" in the tables, an amplified fragment was observed for all

of the genes. The parenthesized numbers after the primer sequences indicate the sequence numbers in Sequence Listing. These primers were used as primers for screening mentioned below.

5

10

15

20

25

30

35

40

45

50

55

Table 2

| Gene | aceA | accBC | dtsRI |
|--|--|--|--|
| 5'→3'Primer | CCTCTATCCAGCGACTCCG (35) | CATCCACCCCGGTACGGCT (37) | ACGGCCCCAGCCCTGACCGAC (39) |
| 3'→5'Primer | CTGCCCTTGAACTCACGGTTC (36) | CGGTGACTGGGTGTTCCACC (38) | AGCAGGCCCCATGACGGCGA (40) |
| PCR conditions for obtaining partial fragment and PCR conditions for screening | 94°C, 5 min 98°C, 5 sec 66°C, 2 sec, 30 cycles Z-Taq | 94°C, 5 min 98°C, 5 sec 66°C, 2 sec, 30 cycles Z-Taq | 94°C, 5 min 98°C, 5 sec 66°C, 2 sec, 30 cycles Z-Taq |
| Conditions of colony PCR | 94°C, 7 min 91°C, 30 sec 55°C, 1 sec 72°C, 2.5 min, 30 cycles Ex-Taq | 94°C, 7 min 91°C, 30 sec 55°C, 1 sec 72°C, 2.5 min, 30 cycles Ex-Taq | 94°C, 7 min 91°C, 30 sec 55°C, 1 sec 72°C, 2.5 min, 30 cycles Ex-Taq |
| Amplified fragment | 824bp | 673bp | 805bp |

Table 3

| Gene | dtSR2 | pfk | scrB |
|--|------------------------------------|----------------------------------|------------------------------------|
| 5'→3' Primer | ACGGCCAGCCCTGACCGAC (41) | CGTCATCCGAGGAATCGTCC (43) | GGNCGHYTBAAYGAYCC (45) |
| 3'→5' Primer | AGCAGCGCCCTGTGACGGGA (42) | CGTGGGGGCCCATGACCTCC (44) | GGRCAYTCCACATRTANCC (46) |
| PCR conditions for obtaining partial fragment and PCR conditions for screening | 94°C, 5 min | 94°C, 5 min | 94°C, 5 min |
| | 98°C, 5 sec | 98°C, 5 sec | 98°C, 5 sec |
| | 66°C, 2 sec, 30 cycles | 66°C, 2 sec, 30 cycles | 50°C, 10 sec |
| | 2-Taq | 2-Taq | 72°C, 20 sec, 40 cycles 2-Taq |
| Conditions of colony PCR | 94°C, 7 min | 94°C 7 min | 94°C, 7 min |
| | 91°C, 30 sec | 91°C 30 sec | 91°C, 30 sec |
| | 55°C, 1 sec | 55°C 1 sec | 55°C, 1 sec |
| | 72°C, 2.5 min, 30 cycles Ex-Taq | 72°C 2.5 min 30 cycles Ex-Taq | 72°C, 2.5 min, 30 cycles Ex-Taq |
| Amplified fragment | 805bp | 472bp | 500bp |

Table 4

| Gene | <i>gluABCD</i> | <i>pdhA</i> |
|---|--|--|
| 5'→3'Primer | CCATCCGGATCCGGCAAGTC (47) | ACTGTGTCCATGGGTCTTGGCCC (49) |
| 3'→5'Primer | AATCCCATCTCGTGGGTAAC (48) | CGCTGGAATCCGAACATCGA (50) |
| PCR conditions for obtaining partial fragment | 94°C, 5 min 98°C, 5 sec 50°C, 10 sec 72°C, 20 sec, 30 cycles Z-Taq | 94°C, 5 min 98°C, 5 sec 50°C, 10 sec 72°C, 20 sec, 30 cycles Z-Taq |
| Amplified fragment | 500bp | 1200bp |
| Conditions for screening PCR and colony PCR | 94°C, 5 min 94°C, 30 sec 50°C, 1 min 72°C, 2 min, 30 cycles EX-Taq | 94°C, 5 min 94°C, 30 sec 50°C, 1 min 72°C, 2 min, 30 cycles EX-Taq |

Table 5

| Gene | pc | ppc |
|---|--|--|
| 5'→3'Primer | GGCGCAACCTACGACGTTGCAATGCG (51) | GGTTCCTGGATTGGTGGAGA(53) |
| 3'→5'Primer | TGGCCGCCTGGGATCTCGTG (52) | CCGCCATCCTTGTGGAATC(54) |
| PCR conditions for obtaining partial fragment | 94°C, 5 min 98°C, 5 sec 55°C, 80 sec 30 cycles Z-Taq | 94°C 5 min 98°C 5 sec 50°C 5 sec 72°C 10 sec 30 cycles Z-Taq |
| Amplified fragment | 781bp | 1000bp |
| Conditions for screening PCR | 94°C, 5 min 98°C, 5 sec 55°C, 80 sec 30 cycles Z-Taq | 94°C, 5 min 98°C, 5 sec 50°C, 5 sec 72°C, 10 sec, 30 cycles Z-Taq |
| Conditions for colony PCR | 94°C, 5 min, 1 cycles 98°C, 5 sec 55°C, 80 sec, 50 cycles Z-Taq | 94°C, 5 min 98°C, 5 sec 50°C, 10 sec 72°C, 20 sec, 50 cycles Z-Taq |

Table 6

| Gene | acn | icd | lpd |
|---|--|--|--|
| 5'→3'Primer | GTIGGIACIGAYTCSCATAC (55) | GACATTTCACCTCGCTGGACG (57) | ATCATCGCAACCGGTTTC (59) |
| 3'→5'Primer | GCIGGAGAIATGTGTCIGT (56) | CCGTACTCTTCAGCCCTTCTG (58) | CGTCACCGATGGCGTAAAT (60) |
| PCR conditions for obtaining partial fragment | 94°C, 1 min 96°C, 20 sec 45°C, 1 min 68°C, 2 min, 30 cycles EX-Taq | 94°C, 5 min 98°C, 5 sec 55°C, 80 sec, 30 cycles Z-Taq | 94°C, 5 min 98°C, 5 sec 50°C, 10 sec 72°C, 20 sec, 30 cycles Z-Taq |
| Amplified fragment | 1500bp | 1500bp | 500bp |
| Conditions for screening PCR and colony PCR | Same as above | Same as above | 94°C, 5 min 94°C, 30 sec 57°C, 1 min 72°C, 1 min, 30 cycles Ex-Taq |
| Screening PCR 5'→3'Primer 3'→5'Primer | | | TACGAGGAGCAGATCCTCAA (63) TTGACGCCGGGTGTTCTCCAG (64) |

Table 6 (Cont.)

| Gene | acn | lcd | Lpd |
|------------------------------------|---|--|--|
| LA cloning (N') 3'→5' primer | S1:GCTGAAGCTAAGTAGTTAGC (65) S2:AGCTACTAAACCTGCACC (66) | S1:CCGTACTCTTCAGCCCTTCTG (67) S2:TCGTCCCTTGTCCACATC (68) | S1:ATCATCGCAACCGGTTTC (69) S2:TACGAGGAGCAGATCCTCAA (70) |
| LA Cloning (C') 5'→3' primer | S1:GCTAACTACTTAGCTTCACC (71) S2:GAACCCAGGAACCTATTGAACC (72) | S1:TCCGATGTCATCATCGAC (73) S2:ATGTGGAACAAGGACGAC (74) | |
| Restriction enzyme | PstI(N') HindIII(C') | Sali(N') PstI(C') | HindIII |
| Conditions for LA cloning | N' 94°C, 1 min 94°C, 30 sec 57°C, 2 min 72°C, 2 min, 30 cycles LA-Taq | 94°C, 1 min 94°C, 30 sec 57°C, 2 min 72°C, 2.5 min, 30 cycles LA-Taq | 94°C, 1 min 94°C, 30 sec 57°C, 2 min 72°C, 1 min, 30 cycles LA-Taq |
| | C' 94°C, 1 min 94°C, 30 sec 57°C, 2 min 72°C, 2.5 min, 30 cycles LA-Taq | | |

Table 7

| Gene | odhA | |
|---|--|---|
| 5'→3'Primer | ACACCGTGGTCGCCTCAACG (61) | |
| 3'→5'Primer | TGCTAACCCGTCCCACCTGG (62) | |
| PCR conditions for obtaining partial fragment | 94°C, 5 min 98°C, 5 sec 66°C, 2 sec, 30 cycles 2-Taq | |
| Amplified fragment | 1306bp | |
| LA cloning (N') 5'→3'Primer | S1:GTACATATTGTCGTTAGAACGCGTAATACGACTCA(75) S2:CGTTAGAACGCGTAATACGACTCACTATAGGGAGA(76) | |
| Restriction | XbaI | |
| Conditions for LA cloning | First time | 94°C, 30 sec 55°C, 2 min 72°C, 1 min 30 cycles LA-Taq |
| | Second time | 94°C, 1 min 98°C, 20 sec 68°C, 15 min, 30 cycles 72°C 10 min LA-Taq |

<3> Screening of plasmid library by PCR

[0097] A clone containing a target gene was selected from the plasmid library by PCR. Sixty colonies were picked up from each plasmid library, and replicated onto two LB agar medium plates. The 60 colonies of each plate were combined, inoculated to a test tube containing 4 ml of LB liquid medium and cultured for 15 hours. Then, a plasmid mixture was respectively obtained by using a plasmid DNA extraction kit produced by Promega. By using this plasmid mixture as a template and primers for screening prepared for each target gene, PCR was performed with the conditions shown as "conditions for screening PCR" in each table to select a clone from which a DNA fragment of the same size as that obtained by PCR using chromosomal DNA as a template had been amplified.

[0098] The nucleotide sequence of the amplified DNA fragment was determined by using a Big Dye dye terminator cycle sequencing kit produced by Perkin-Elmer, and investigating its homology to known gene information to determine if the target gene was obtained or not.

[0099] As for *lpa*, since any DNA fragment was not amplified with the primers produced in <2>, other primers for screening were prepared based on the determined nucleotide sequence.

<4> Selection of clone harboring target gene by colony PCR

[0100] By using a plate that was an origin of a plasmid mixture for which amplification of the target gene fragment was confirmed, colony PCR was performed to select a clone containing the gene fragment. The colony PCR was performed with the conditions shown in Tables 2-7.

[0101] Plasmid DNA was collected from a selected transformant and the nucleotide sequence of the inserted DNA fragment was determined. When the full length of the target gene was not inserted in the inserted DNA fragment, and a upstream region, downstream region or the both were deleted, primers were prepared based on the determined nucleotide sequence, with which a gene fragment comprising the nucleotide sequence of the target gene in its full length was obtained by using TaKaRa LA PCR in vitro Cloning Kit (Takara Shuzo). Then, its nucleotide sequence was determined.

[0102] The outline of LA PCR cloning was as follows. Two kinds of primers each having one of the nucleotide sequences of two regions of the inserted DNA fragment were produced. Chromosomal DNA of *Corynebacterium thermoaminogenes* AJ12310 strain was digested with various restriction enzymes, and ligated to a cassette primer corresponding to each of the restriction enzymes. By using this as a template, PCR was performed with a primer (S1) corresponding to a position distant from the deletion region and a cassette primer (C1) corresponding to a position outside the cassette primer among the prepared primers. Then, another PCR was performed with a primer (S2) corresponding to a position near the deletion region and a cassette primer (C2) corresponding to a position inside the cassette primer among the prepared primers. In this way, a DNA fragment containing the deleted region was obtained. By ligating the obtained DNA fragment with the already obtained DNA fragment, a DNA fragment containing the target gene in full length could be obtained. Since 5' end of the cassette did not have a phosphate group, a nick was formed at the ligation site of the 3' end of the DNA fragment and the 5' end of the cassette. Therefore, the DNA synthesis from the primer C1 stopped at this ligation site in the first PCR, and thus non-specific amplification did not occur. Therefore, specific amplification could be attained.

[0103] The primers and the reaction conditions used for the LA PCR cloning are shown in Tables 2-7. In the tables, the primers mentioned with "(N)" are primers used for the cloning of an upstream deleted portion, and the primers mentioned with "(C)" are primers used for the cloning of a downstream deleted portion. PCR was performed twice according to the instruction attached to the LA PCR cloning kit. Among the primers mentioned in the tables, the primers (S1) used for the first reaction are shown in the upper row, and the primers (S2) used for the second reaction are shown in the lower row.

[0104] The nucleotide sequences of the DNA fragments containing each gene obtained as described above were determined in the same manner as mentioned above. Those nucleotide sequences and amino acid sequences that can be encoded by those nucleotide sequences are shown in SEQ ID NOS: 1-34. The sequences shown with the sequence numbers are summarized in Explanation of Sequence Listing mentioned hereinafter.

[0105] As for *scrB*, any open reading frame was not found. Since the *Corynebacterium thermoaminogenes* AJ12310 strain did not have the invertase activity and did not have sucrose assimilating property, an *scrB* gene fragment was obtained in a similar manner from *Corynebacterium thermoaminogenes* AJ12340 and AJ12309 strains having the sucrose assimilating property. As a result, a DNA fragment having an open reading frame was obtained from the both strains.

Example 2: Acquisition of *gdh* and *gltA* gene

<1> Investigation of GDH activity of *Corynebacterium thermoaminogenes*

[0106] Cells of a wild strain of *Corynebacterium thermoaminogenes*, the AJ12310 strain, was grown on CM-2B agar medium (1 g/dl of yeast extract (produced by Difco), 1 g/dl of polypeptone (produced by Nippon Seiyaku), 0.5 g/dl of NaCl, 10 µg/dl of biotin, 1.5 g/dl of agar, adjusted to pH 7.0 with KOH). The cells were inoculated to a 500-ml volume flask containing 20 ml of a medium for flask having the following composition and cultured at 37°C for 17 hours (until the residual sugar reached about 1 g/dl).

[0107] Similarly, cells of the 2256 strain (ATCC13869) of *Brevibacterium lactofermentum* grown on CM-2B agar medium were cultured at 31.5°C for 17 hours.

[Medium for flask]

[0108]

| | |
|---------|--------|
| Glucose | 3 g/dl |
|---------|--------|

(continued)

| | | |
|----|---|-----------|
| | KH ₂ PO ₄ | 0.1 g/dl |
| | MgSO ₄ ·H ₂ O | 0.04 g/dl |
| 5 | FeSO ₄ ·7H ₂ O | 1 mg/dl |
| | MnSO ₄ ·4H ₂ O | 1 mg/dl |
| | Vitamin B ₁ -HCl | 200 µg/L |
| | Biotin | 50 µg/L |
| 10 | (NH ₄) ₂ SO ₄ | 1.5 g/dl |
| | Soybean protein hydrolysis solution (Memenó (T-N)) | 48 mg/dl |
| | CaCO ₃ (Official reagent) (separately sterilized) | 5 g/dl |
| 15 | pH 8.0 (adjusted with KOH) | |

[0109] About 1 ml of the above culture medium was centrifuged at 1000 rpm for 1 minute to remove CaCO₃, and the cells were washed twice with 200 mM K-phosphate buffer (pH 6.9) and suspended in 300 µl of the same buffer. The obtained cell suspension was sonicated for 5 minutes to disrupt the cells, centrifuged at 1000 rpm for 30 minutes to obtain a crude enzyme solution as the supernatant.

[0110] The optimum reaction temperature and the thermal stability of GDH activity were investigated using the aforementioned crude enzyme solution. The measurement of GDH activity was performed by adding the crude enzyme solution to a reaction mixture (100 mM Tris-HCl (pH 8.0), 20 mM NH₄Cl, 10 mM sodium α-ketoglutarate, 0.25 mM NADPH) and measuring change of absorbance at 340 nm. The protein concentration of the crude enzyme solution was quantified by the Bradford method (Bio-Rad Protein Assay Kit was used) using bovine serum albumin as the standard through measurement of absorbance at 595 nm. The absorbance was measured by using HITACHI U-2000 (produced by Hitachi).

[0111] The GDH activity measured at various reaction temperatures is shown in Fig. 1. While the ATCC13869 strain showed the highest specific activity of GDH around 37°C and the activity markedly decreased around 42°C, the AJ12310 strain showed the highest specific activity around 42°C and it showed the activity even at 45°C.

[0112] Then, the thermal stability of GDH was investigated. The crude enzyme solution was left at 65°C for 0 to 30 minutes before the reaction, and then the enzyme activity was measured at 30°C. The results are shown in Fig. 2. As clearly seen from the results, while GDH of the ATCC13869 strain was inactivated by the heat treatment for 5 minutes, GDH of the AJ12310 strain maintained the activity even after the heat treatment for 30 minutes. In addition, the crude enzyme solution of the AJ12310 strain showed substantially no change in the GDH activity even after the heat treatment at 65°C for 90 minutes (data are not shown).

<2> Examination of CS activity of *Corynebacterium thermoaminogenes*

[0113] The optimum reaction temperature and thermal stability of CS were investigated by using crude enzyme solutions prepared from the cells of the *Corynebacterium thermoaminogenes* AJ12310 strain and the *Brevibacterium lactofermentum* ATCC13869 strain in the same manner as in Example 1. The measurement of CS activity was performed by adding each crude enzyme solution to a reaction mixture (100 mM Tris-HCl (pH 8.0), 0.1 mM DTNB (5,5'-dithiobis-(2-nitrobenzoic acid)), 200 mM sodium L-glutamate, 0.3 mM acetyl CoA), and measuring change of the absorbance at 412 nm.

[0114] The CS activity measured at various reaction temperatures is shown in Fig. 3. The ATCC13869 strain showed the highest specific activity of CS around 23°C and the activity markedly decreased around 33°C. However, the AJ12310 strain showed high specific activity in a reaction temperature-dependent manner up to around 37°C and it showed the activity even at 40°C in a degree corresponding to about 40% of the activity at 37°C.

[0115] Then, thermal stability of CS was investigated. The crude enzyme solution was left at 33-55°C for 5 minutes before the reaction, and then the enzyme activity was measured at 30°C. The results are shown in Fig. 4. Whereas CS of the ATCC13869 strain was inactivated by the heat treatment at 35-40°C, CS of the AJ12310 strain maintained about 40% of the activity even after the heat treatment at 50°C.

<3> Acquisition of *gdh* gene of *Corynebacterium thermoaminogenes*

[0116] The already reported nucleotide sequences of *gdh* gene of various microorganisms were compared. A region

in which nucleotide sequences were well conserved was selected, and primers having the nucleotide sequences shown in SEQ ID NOS: 77 and 78 were prepared based on the nucleotide sequence of the region.

[0117] PCR was performed by using chromosomal DNA prepared from the *Corynebacterium thermoaminogenes* AJ12310 strain using Bacterial Genome DNA Purification Kit (produced by Advanced Genetic Technologies) as a template and the aforementioned primers. Based on the obtained DNA fragment, genome walking was performed by using TaKaRa LA PCR in vitro Cloning Kit (produced by Takara Shuzo) to obtain the whole *gdh* gene, of which whole nucleotide sequence was determined. The result is shown in SEQ ID NO: 79. Further, the amino acid sequence deduced from this nucleotide sequence is shown in SEQ ID NO: 80.

[0118] The *gdh* gene of the *Brevibacterium lactofermentum* ATCC13869 strain was obtained in a similar manner, and its nucleotide sequence was determined. The result is shown in SEQ ID NO: 81. The amino acid sequence encoded by this nucleotide sequence is shown in SEQ ID NO: 82.

[0119] Homology was investigated for the nucleotide sequences of the *gdh* gene and the amino acid sequences of GDH of the *Corynebacterium thermoaminogenes* AJ12310 strain and the *Brevibacterium lactofermentum* ATCC13869 strain determined as described above, and the known *gdh* gene and amino acid sequence of GDH of the *Corynebacterium glutamicum* (C. *glutamicum*) ATCC13032 strain (Molecular Microbiology 6, 317-326 (1992)). The results are shown in Table 8 (for nucleotide sequences) and Table 9 (for amino acid sequences).

Table 8:

| Homology of nucleotide sequences of various <i>gdh</i> genes | | | |
|--|-----------|-----------|---------|
| | ATCC13869 | ATCC13032 | AJ12310 |
| ATCC13869 | - | 94.5% | 82.4% |
| ATCC13032 | - | - | 78.1% |
| AJ12310 | - | - | - |

Table 9:

| Homology of amino acid sequences of various GDH | | | |
|---|-----------|-----------|---------|
| | ATCC13869 | ATCC13032 | AJ12310 |
| ATCC13869 | - | 90.8% | 91.7% |
| ATCC13032 | - | - | 83.4% |
| AJ12310 | - | - | - |

<4> Acquisition of *gltA* gene of *Corynebacterium thermoaminogenes*

[0120] The already reported nucleotide sequences of *gltA* gene of various microorganisms were compared. A region in which nucleotide sequences were well conserved was selected, and primers having the nucleotide sequences shown in SEQ ID NOS: 83 and 84 were prepared based on the nucleotide sequence of the region.

[0121] PCR was performed by using chromosomal DNA prepared from the *Corynebacterium thermoaminogenes* AJ12310 strain (FERM BP-1542) using Bacterial Genome DNA Purification Kit (produced by Advanced Genetic Technologies) as a template and the aforementioned primers 7 and 8, and the nucleotide sequence of the amplified nucleotide sequence of about 0.9 kb was determined.

[0122] On the basis of the obtained nucleotide sequence of *gltA* gene of *Corynebacterium glutamicum* (Microbiol., 140, 1817-1828 (1994)), the primers of SEQ ID NOS: 85, 86, 87 and 88 were prepared. PCR was performed in a manner similar to the above by using chromosomal DNA of AJ12310 as a template and the primers of SEQ ID NOS: 85, 86, 87 and 88, and the nucleotide sequence of the amplified DNA fragment was specified to determine the whole nucleotide sequence of the *gltA* gene. The result is shown in SEQ ID NO: 89. Further, an amino acid sequence expected from this nucleotide sequence is shown in SEQ ID NO: 90.

[0123] The *gltA* gene of the *Brevibacterium lactofermentum* 2256 strain was obtained in a similar manner, and its nucleotide sequence was determined. The result is shown in SEQ ID NO: 91. The amino acid sequence encoded by this nucleotide sequence is shown in SEQ ID NO: 92.

[0124] Homology was investigated for the nucleotide sequences of the *gltA* gene and the amino acid sequences of CS of the *Corynebacterium thermoaminogenes* AJ12310 strain and the *Brevibacterium lactofermentum* ATCC13032 strain determined as described above, and the known *gltA* gene and amino acid sequence of CS of the *Corynebacterium*

glutamicum ATCC13032 strain (*Microbiol.* 140, 1817-1828 (1994)). The results are shown in Table 10 (for nucleotide sequences) and Table 11 (for amino acid sequences).

Table 10:

| Homology of nucleotide sequences of various <i>gltA</i> genes | | | |
|---|-----------|-----------|---------|
| | ATCC13869 | ATCC13032 | AJ12310 |
| ATCC13869 | - | 99.5% | 85.7% |
| ATCC13032 | - | - | 85.6% |
| AJ12310 | - | - | - |

Table 11:

| Homology of amino acid sequences of various CS | | | |
|--|-----------|-----------|---------|
| | ATCC13869 | ATCC13032 | AJ12310 |
| ATCC13869 | - | 99.3% | 92.1% |
| ATCC13032 | - | - | 92.1% |
| AJ12310 | - | - | - |

Example 3: Acquisition of *scrB* gene of *Corynebacterium thermoaminogenes*

[0125] Since an *scrB* gene fragment was obtained from the *Corynebacterium thermoaminogenes* AJ12309 strain as shown in Example 1, it was attempted to obtain the total sequence of the gene. First, a partial fragment was obtained in the same manner as in Example 1 using the primers shown in SEQ ID NO: 45 and SEQ ID NO: 46. These primers were synthesized based on the *scrB* sequence of the *Brevibacterium lactofermentum* 2256 strain (Japanese Patent Laid-open No. 08-196280/1996).

[0126] Separately, chromosomal DNA was prepared from the AJ12309 strain by using Bacterial Genome DNA Purification Kit (Advanced Genetic Technologies Corp.). Sterilized water was added to 0.5 µg of this chromosomal DNA, 50 pmol each of the aforementioned primers, 4 µl of dNTP mixture (2.5 mM each), 5 µl of 10 x Z-Taq Buffer (Takara Shuzo) and 2 U of Z-Taq (Takara Shuzo) to prepare a PCR reaction mixture in a total volume of 50 µl. PCR was performed with a cycle of denaturation at 98°C for 5 seconds, association at 50°C for 10 seconds and extension reaction at 72°C for 20 seconds, which was repeated for 30 cycles, by using the above reaction mixture and a thermal cycler GeneAmp PCR System 9600 (PE) to amplify a partial fragment of *scrB* of about 600 bp.

[0127] Then, the total sequence of *scrB* was determined by using an LA PCR in vitro Cloning Kit (Takara Shuzo). All of the procedure was performed in accordance with the protocol attached to the LA PCR in vitro Cloning Kit. Based on the obtained partial sequence, primers shown in SEQ ID NOS: 97, 98, 99 and 100 were synthesized. For the first PCR reaction for sequencing an upstream region, the primers shown in SEQ ID NOS: 95 and 97 and chromosomal DNA of AJ12309 strain digested with *EcoT14I* as a template DNA were used. For the second PCR reaction, the primers shown in SEQ ID NOS: 96 and 98 were used. For the first PCR reaction for sequencing a downstream region, the primers shown in SEQ ID NOS: 95 and 99 and chromosomal DNA of AJ12309 strain digested with *SalI* (Takara Shuzo) as a template DNA were used. For the second PCR reaction, the primers shown in SEQ ID NOS: 96 and 100 were used. By the above procedure, a sequence of a full length of 1656 bp containing ORF of *scrB* was determined. This nucleotide sequence is shown in SEQ ID NO: 93, and a deduced amino acid sequence is shown in SEQ ID NO: 94.

Example 4: Examination of thermal stability of isocitrate lyase, phosphofructokinase, phosphoenolpyruvate carboxylase, aconitase, isocitrate dehydrogenase and 2-oxoglutarate dehydrogenase

[0128] Thermal stability was investigated for the following enzymes derived from *Corynebacterium thermoaminogenes*. In this Example, protein concentrations were measured by the Bradford method (Bio-Rad Protein Assay Kit was used) using bovine serum albumin as a standard protein. Further, measurement of absorbance was performed by using HITACHI U-2000 (Hitachi) unless otherwise indicated.

<1> Isocitrate lyase

[0129] Thermal stability of activity of isocitrate lyase (henceforth also referred to as "ICL") derived from the *Corynebacterium thermoaminogenes* AJ12310 strain and ICL derived from the *Brevibacterium lactofermentum* 2256 strain (ATCC13869) was investigated. For the activity measurement, used were cells of which culture in a medium having the composition mentioned in Table 2 was terminated before all of the carbon source was completely consumed. The method of the activity measurement was one described in Dieter J. Reinscheid *et al.*, *J. Bacteriol.*, 176 (12), 3474 (1994). Specifically, the cells were washed with 50 mM Tris buffer (pH 7.3), suspended in the same buffer, and disrupted by sonication (INSONATOR 201M produced by KUBOTA was used, 200 W, 5 minutes). After the sonication, the suspension was centrifuged (13000 x g, 30 minutes) to remove undisrupted cells to prepare a crude enzyme solution.

[0130] The crude enzyme solution was added to a reaction system containing 50 mM MOPS-NaOH (pH 7.3), 5 mM dithiothreitol, 15 mM MgCl₂, 1 mM EDTA, 5 mM D-threo-isocitrate, 0.2 mM NADH and 18 U of LDH (lactate dehydrogenase), and absorbance at 340 nm at various temperatures (30, 40, 50, 60 or 70°C) was measured by a Hitachi spectrophotometer U-3210. The measurement results for various reaction temperatures were shown in Fig. 5. Further, the crude enzyme solution was pretreated at 50°C (pretreatment time: 5 minutes or 15 minutes), and the activity was measured at 37°C. The results are shown in Fig. 6.

[0131] As a result, ICL of the AJ12310 strain showed the maximum activity at 60°C, whereas ICL of the 2256 strain showed the maximum activity around 50°C. Further, while ICL of the 2256 strain was completely inactivated after the pretreatment for 5 minutes, ICL of the AJ12310 strain maintained half of the activity after the pretreatment for 5 minutes. Thus, the stability of ICL of the AJ12310 strain at high temperatures was confirmed.

Table 12

| Composition of medium for ICL activity measurement | |
|--|---------------|
| Component | Concentration |
| (NH ₄) ₂ SO ₄ | 5 g/l |
| Urea | 5 g/l |
| KH ₂ PO ₄ | 0.5 g/l |
| K ₂ HPO ₄ | 0.5 g/l |
| MOPS | 20.9 g/l |
| MgSO ₄ ·7H ₂ O | 0.25 g/l |
| CaCl ₂ ·7H ₂ O | 10 mM |
| CuSO ₄ ·7H ₂ O | 0.2 mg/l |
| Biotin | 0.2 mg/l |
| MnSO ₄ ·7H ₂ O | 10 mg/l |
| FeSO ₄ ·7H ₂ O | 10 mg/l |
| ZnSO ₄ ·7H ₂ O | 1 mg/l |
| Acetic acid | 4% |

<2> Phosphofructokinase

[0132] Thermal stability of activity of phosphofructokinase (henceforth also referred to as "PKF") derived from the *Corynebacterium thermoaminogenes* AJ12310 strain and PKF derived from the *Brevibacterium lactofermentum* 2256 strain was investigated. For the activity measurement, used were cells of which culture in a medium having the composition mentioned in Table 13 was terminated before all of the saccharide was completely consumed. The method of the activity measurement was one described in Michiko Mori *et al.*, *Agric. Biol. Chem.*, 51 (10), 2671 (1994). Specifically, the cells were washed with 0.1 M Tris buffer (pH 7.5), suspended in the same buffer, and disrupted by sonication (INSONATOR 201M produced by KUBOTA was used, 200 W, 5 minutes). After the sonication, the suspension was centrifuged (13000 x g, 30 minutes) to remove undisrupted cells to obtain a crude enzyme solution.

[0133] The crude enzyme solution was added to a reaction system containing 100 mM Tris buffer (pH 7.5), 0.2 mM NADH, 10 mM MgCl₂, 2 mM NH₄Cl, 10 mM KCl, 0.2 mM phosphoenolpyruvic acid, 6.4 mM fructose-6-phosphate, 1 mM ATP and 40 µg of LDH/PK (pyruvate kinase), and absorbance at 340 nm was measured at various temperatures

(30, 40, 50, 60 or 70°C) by a Hitachi spectrophotometer U-3210. The measurement results for various reaction temperatures were shown in Fig. 7. Further, the crude enzyme solution was pretreated at 50°C (pretreatment time: 1, 3, 5 or 10 minutes), and the activity was measured at 37°C. The results are shown in Fig. 8.

[0134] As a result, PKF of the AJ12310 strain showed the maximum activity around 50°C, whereas PKF of the 2256 strain showed the maximum activity around 30°C. Thus, it was confirmed that the optimum temperature of PKF of the AJ12310 strain resided in a high temperature region.

Table 13

| Composition of medium for PFK activity measurement | |
|--|---------------|
| Component | Concentration |
| Polypeptone | 20 g/l |
| Yeast extract | 20 g/l |
| Sodium chloride | 5 g/l |
| Glucose | 20 g/l |

<3> Phosphoenolpyruvate carboxylase

[0135] Thermal stability of activity of phosphoenolpyruvate carboxylase (henceforth also referred to as "PEPC") derived from the *Corynebacterium thermoaminogenes* AJ12310 strain and PEPC of the *Brevibacterium lactofermentum* 2256 strain was examined.

[0136] Cells of the AJ12310 strain grown on CM-2B agar medium were inoculated to a 500-ml volume flask containing 20 ml of a medium for flask (8 g/dl of Glucose, 0.1 g/dl of KH_2PO_4 , 0.04 g/dl of $\text{MgSO}_4 \cdot \text{H}_2\text{O}$, 1 mg/dl of $\text{FeSO}_4 \cdot 7\text{H}_2\text{O}$, 5 mg/dl of $\text{MnSO}_4 \cdot 4\text{H}_2\text{O}$, 3 g/dl of $(\text{NH}_4)_2\text{SO}_4$, 48 mg/dl of TN (soybean protein hydrolysis solution), 200 µg/L of vitamin B₁, 300 µg/L of biotin, 50 µl/l of GD-113 (antifoaming agent), 5 g/dl of CaCO_3 (Official reagent, separately sterilized), pH 8.0 (adjusted with KOH)), and cultured at 37°C. Cells of the 2256 strain grown on CM-2B agar medium were similarly cultured at 31.5°C.

[0137] The above culture broth in which the cells were grown to the logarithmic growth phase was centrifuged at 1000 rpm for 1 minute to remove CaCO_3 , and the cells were washed 3 times with washing buffer (100 mM Tris/HCl pH 8.0, 10 mM MgSO_4 , 1 mM DTT, 20% glycerol), sonicated to disrupt the cells, and centrifuged at 15 krpm for 10 minutes to remove cell debris. The supernatant was further centrifuged at 60 krpm for 1 hour to obtain a crude enzyme solution as the supernatant.

[0138] By using the above crude enzyme solution, optimum reaction temperature and thermal stability of the PEPC activity were investigated. The measurement of PEPC activity was performed by adding the crude enzyme solution to a reaction mixture (100 mM Tris/ H_2SO_4 (pH 8.5), 5 mM phosphoenolpyruvic acid, 10 mM KHCO_3 , 0.1 mM acetyl-CoA, 0.15 mM NADH, 10 mM MgSO_4 , 10 U of malate dehydrogenase, 0.1 mM DTT), and measuring change of the absorbance at 340 nm in 800 µl of reaction volume.

[0139] The PEPC activity measured at various reaction temperatures is shown in Fig. 9. While the activity of the 2256 strain markedly decreased at 40°C, the AJ12310 strain showed substantially no decrease of the activity even at 40°C.

[0140] Then, the thermal stability of PEPC was investigated. The crude enzyme solution was left at 45°C for 0-20 minutes before the reaction, and then the enzyme activity was measured at 20°C. The results are shown in Fig. 10. As clearly seen from the results, whereas the PEPC activity of the 2256 strain was substantially lost after the heat treatment for 10 minutes, PEPC of the AJ12310 strain maintained the activity even after the heat treatment for 20 minutes.

[0141] These results demonstrated the stability of PEPC of the AJ12310 strain at a high temperature.

<4> Aconitase

[0142] Aconitase (henceforth also referred to as "ACN") derived from the *Corynebacterium thermoaminogenes* AJ12310 strain and ACN derived from the *Brevibacterium lactofermentum* 2256 strain were measured, and thermal stability thereof was examined.

[0143] Cells of the AJ12310 strain grown on CM-2B agar medium were inoculated to a 500-ml volume flask containing 20 ml of a medium for flask having the same composition as mentioned in <3>, and cultured at 37°C. Cells of the 2256 strain grown on CM-2B agar medium were similarly cultured at 31.5°C.

[0144] The above culture broth in which the cells were grown to the logarithmic growth phase was centrifuged at

1000 rpm for 1 minute to remove CaCO_3 , and the cells were washed 3 times with 50 mM Tris/HCl pH 7.5, sonicated to disrupt the cells, and centrifuged at 15 krpm for 10 minutes to obtain a crude enzyme solution as the supernatant.

[0145] By using the above crude enzyme solution, optimum reaction temperature and thermal stability of ACN activity were investigated. The measurement of ACN activity was performed by adding the crude enzyme solution to a reaction mixture (20 mM Tris/HCl (pH 7.5), 50 mM NaCl, 20 mM isocitrate-3Na), and measuring change of the absorbance at 240 nm in 800 μl of reaction volume.

[0146] The ACN activity measured at various reaction temperatures is shown in Fig. 11. The AJ12310 strain showed higher activity at a higher temperature compared with the 2256 strain.

[0147] Then, the thermal stability of ACN was investigated. The crude enzyme solution was left at 50°C for 0-15 minutes before the reaction, and then the enzyme activity was measured at 30°C. The results are shown in Fig. 12. As clearly seen from the results, ACN of the AJ12310 strain showed less activity decrease due to the heat treatment compared with ACN of the 2256 strain.

[0148] These results demonstrated the stability of ACN of the AJ12310 strain at a high temperature.

<5> Isocitrate dehydrogenase

[0149] Thermal stability of activity of isocitrate dehydrogenase (henceforth also referred to as "ICDH") derived from the *Corynebacterium thermoaminogenes* AJ12310 strain and ICDH derived from the *Brevibacterium lactofermentum* 2256 strain was examined.

[0150] Cells of the AJ12310 strain grown on CM-2B agar medium were inoculated to a 500-ml volume flask containing 20 ml of a medium for flask having the same composition as mentioned in <3>, and cultured at 37°C. Cells of the 2256 strain grown on CM-2B agar medium were similarly cultured at 31.5°C.

[0151] The above culture broth in which the cells were grown to the logarithmic growth phase was centrifuged at 1000 rpm for 1 minute to remove CaCO_3 , and the cells were washed 3 times with 50 mM Tris/HCl pH 7.5, sonicated to disrupt the cells, and centrifuged at 15 krpm for 10 minutes to obtain a crude enzyme solution as the supernatant.

[0152] By using the above crude enzyme solution, optimum reaction temperature and thermal stability of ICDH activity were investigated. The measurement of ICDH activity was performed by adding the crude enzyme solution to a reaction mixture (35 mM Tris/HCl, 0.35 mM EDTA (pH 7.5), 1.5 mM MnSO_4 , 0.1 mM NADP, 1.3 mM isocitrate-3Na), and measuring change of the absorbance at 340 nm in 800 μl of reaction volume.

[0153] The ICDH activity measured at various reaction temperatures is shown in Fig. 13. While the activity of the 2256 strain markedly decreased at 70°C, substantially no activity decrease was observed even at 70°C for the AJ12310 strain.

[0154] Then, the thermal stability of ICDH was investigated. The crude enzyme solution was left at 45°C for 0-15 minutes before the reaction, and then the enzyme activity was measured at 30°C. The results are shown in Fig. 14. As clearly seen from the results, while only about 15% of residual activity was observed after the heat treatment for 15 minutes for the 2256 strain, about 60% of residual ICDH activity was observed for the AJ12310 strain.

[0155] These results demonstrated the stability of ICDH of the AJ12310 strain at a high temperature.

<6> 2-Oxoglutarate dehydrogenase

[0156] 2-Oxoglutarate dehydrogenase (henceforth also referred to as "ODHC") derived from the *Corynebacterium thermoaminogenes* AJ12310 strain and ODHC derived from the *Brevibacterium lactofermentum* 2256 strain were measured, and thermal stability thereof was examined.

[0157] For the activity measurement, used were cells of which culture in a medium having the composition mentioned in Table 14 was terminated before all of the saccharide was completely consumed. The method of the activity measurement was one described in Isamu Shio et al., Agric. Biol. Chem., 44 (8), 1897 (1980). Specifically, the cells were washed with 0.2% potassium chloride, suspended in 100 mM TES-NaOH (pH 7.5), 30% glycerol solution, and disrupted by sonication (INSONATOR 201M produced by KUBOTA was used, 200 W, 5 minutes). After the disruption by sonication, the suspension was centrifuged (13000 x g, 30 minutes) to remove undisrupted cells, and subjected to gel filtration using the same buffer and Sephadex-G25 to prepare a crude enzyme solution.

[0158] The crude enzyme solution was added to a reaction system containing 100 mM TES-NaOH (pH 7.7), 5 mM MgCl_2 , 0.2 mM Coenzyme A, 0.3 mM cocarboxylase, 1 mM α -ketoglutaric acid, 3 mM L-cysteine and 1 mM acetylpyridine-adenine dinucleotide, and absorbance at 365 nm was measured at various temperatures (30, 40, 50, 60 or 70°C) by a Hitachi spectrophotometer U-3210. The crude enzyme solution was pretreated at 50°C (pretreatment time: 1, 3, 5 or 10 minutes), and the activity was measured at 37°C. The results are shown in Fig. 15.

[0159] As a result, while ODHC of the 2256 strain was completely inactivated by the pretreatment for 10 minutes, ODHC of the AJ12310 strain showed substantially constant activity irrespective of the pretreatment time, and thus its stability against high temperature treatment was confirmed.

Table 14

| Composition of medium for ODHC activity measurement | |
|---|---------------|
| Component | Concentration |
| Glucose | 80 g/l |
| KH ₂ PO ₄ | 1 g/l |
| MgSO ₄ ·7H ₂ O | 0.4 g/l |
| FeSO ₄ ·7H ₂ O | 0.01 g/l |
| MnSO ₄ ·7H ₂ O | 0.05 g/l |
| (NH ₄) ₂ SO ₄ | 30 g/l |
| rotein Soybean protein hydrolysate | 480 mg/l |
| Thiamin hydrochloride | 200 µg/l |
| Biotin | 300 µg/l |

Example 5: Impartation of sucrose assimilating ability by gene transfer of *scrB* gene

[0160] Since the *Corynebacterium thermoaminogenes* AJ12310 strain did not have invertase activity and sucrose assimilating property, it was investigated if sucrose assimilating ability could be imparted to it by transferring the *scrB* gene of the AJ12309 strain to the strain.

<1> Production of plasmid carrying *scrB* derived from *Corynebacterium thermoaminogenes* AJ12309 strain

[0161] To obtain an *scrB* gene fragment, the primers shown in SEQ ID NOS: 101 and 102 were synthesized, of which both ends were ligated with *Sma*I sequences, based on the nucleotide sequence shown in SEQ ID NO: 93. Sterilized water was added to 0.5 µg of chromosomal DNA of the 12309 strain, 50 pmol each of the aforementioned oligonucleotides, 4 µl of dNTP mixture (2.5 mM each), 5 µl of 10 x Pyrobest Buffer (Takara Shuzo) and 2 U of Pyrobest polymerase (Takara Shuzo) to prepare a PCR reaction mixture in a total volume of 50 µl. PCR was performed with a cycle of denaturation at 98°C for 10 seconds, association at 55°C for 30 seconds and extension reaction at 72°C for 2 minutes, which was repeated for 30 cycles, by using the above reaction mixture and a thermal cycler GeneAmp PCR System 9600 (PE) to amplify a fragment of about 1.7 kb containing *scrB* ORF.

[0162] Then, the above amplified fragment was digested with *Sma*I (Takara Shuzo), and ligated to plasmid pSAC4 containing a dephosphorylated replication origin functioning in coryneform bacteria, which had been digested with *Sma*I, to prepare pSCR155. The construction of pSCR155 is shown in Fig. 16. pSAC4 was produced as follows. In order to make the vector for *Escherichia coli* pHSG399 (Takara Shuzo) autonomously replicable in coryneform bacteria, the replication origin (Japanese Patent Laid-open No. 5-7491/1993) derived from the already obtained plasmid pHM1519 autonomously replicable in coryneform bacteria (Miwa, K. et al., Agric. Biol. Chem., 48 (1984) 2901-2903) was introduced into it. Specifically, pHM1519 was digested with restriction enzymes *Bam*HI and *Kpn*I, and the obtained fragment containing the replication origin was blunt-ended by using a Blunting kit produced by Takara Shuzo and inserted into pHSG399 at the *Sal*I site by using an *Sal*I linker (produced by Takara Shuzo) to obtain pSAC4.

<2> Transfer of plasmid carrying *scrB* gene into AJ12310 strain

[0163] pSCR155 produced above and plasmid pSSM30BS (Japanese Patent Laid-open No. 08-196280/1996) carrying the *scrB* gene derived from *Brevibacterium lactofermentum* were introduced into the *Corynebacterium thermoaminogenes* AJ12310 strain. The transformation was performed according to the following procedure. The cells were inoculated to CM-2B medium containing 20% sucrose in such an amount that OD₆₆₀ of the medium should become 0.1, and cultured at 37°C with shaking until the OD₆₆₀ become 0.3. Lysozyme was added to the medium at a concentration of 100 µg/ml, and the cells were further cultured for 2 hours. The cells were washed three times with 20% sucrose, suspended in 20% sucrose, added with the plasmid collected from *Escherichia coli* JM110, mixed sufficiently, and applied with an electric pulse (18 kV/cm, 300 msec) to be introduced with the DNA. After the cells were subjected to restoration culture overnight in CM-2B medium containing 20% sucrose, transformants were selected on CM-2B agar medium containing 5 µg/ml of chloramphenicol. Specifically, the transformation was performed by the electric pulse method (Japanese Patent Laid-open No. 12-204236/2000, and the selection of transformants was performed

on CM2B plate medium containing 5 µg/ml of chloramphenicol at 37°C. As a result, any transformant harboring the plasmid pSSM30BS carrying *scrB* derived from *Brevibacterium lactofermentum* was not obtained, but only a transformant harboring the plasmid pSCR155 carrying *scrB* derived from *Corynebacterium thermoaminogenes* was obtained. This strain was designated as AJ12310/pSCR155.

<3> Evaluation of culture of AJ12310/pSCR155 strain using sucrose as sugar source.

[0164] AJ12310/pSCR155 prepared above was inoculated to a medium having the composition shown in Table 15, and cultured at 37°C for 22 hours with shaking. The absorbance (OD) and residual sugar (RS) of the medium were measured after the culture. The results are shown in Table 16. As a result, it was confirmed that, while the AJ12310 strain could not assimilate sucrose and hence could not grow, the *scrB* gene introduced strain, the AJ12310/pSCR155 strain, became to be able to assimilate sucrose.

Table 15

| Medium composition | |
|---|---------------|
| Medium composition | Concentration |
| Sucrose | 60 g/l |
| KH ₂ PO ₄ | 1 g/l |
| MgSO ₄ ·7H ₂ O | 0.4 g/l |
| FeSO ₄ ·7H ₂ O | 0.01 g/l |
| MnSO ₄ ·7H ₂ O | 0.01 g/l |
| (NH ₄) ₂ SO ₄ | 30 g/l |
| Soybean protein hydrolysate | 480 mg/l |
| Thiamin hydrochloride | 200 µg/l |
| Biotin | 300 µg/l |

Table 16

| Result of sucrose culture | | |
|---------------------------|-----------|----------|
| | OD (x 51) | RS (g/l) |
| 2256 | 1.292 | 0.00 |
| AJ12310 | 0.058 | 60.00 |
| AJ12310/pSCR155 | 1.571 | 0.84 |

Example 6: L-glutamic acid production by *pdhA* gene-amplified strain

<1> Construction of plasmid pPDHA-2 carrying *pdhA*

[0165] The *pdhA* gene derived from the *Corynebacterium thermoaminogenes* AJ12310 strain was obtained by screening of a plasmid library. Specifically, PCR was performed with the conditions shown in Example 1, Table 4, using a plasmid library mixture as a template, and a clone p21A was selected, from which a DNA fragment of the same size is amplified as obtained in PCR using chromosomal DNA as a template. The DNA sequence of this plasmid was determined to confirm that the full length of *pdhA* was contained in it.

[0166] p21A was digested with *Xba*I and *Kpn*I to excise a DNA fragment of 4 kb containing the full length of the *pdhA* gene and a promoter region. This DNA fragment containing the *pdhA* gene was inserted into the *Xba*I and *Kpn*I sites of pHSG299 (Takara Shuzo). Then, this plasmid was digested with *Xba*I, and a fragment obtained by digesting pXK4 with *Xba*I was inserted to prepare pPDHA-2. The construction process of pPDHA-2 is shown in Fig. 17. A DNA Ligation Kit Ver.2 (Takara Shuzo) was used for the ligation reaction, and *Escherichia coli* JM109 strain (Takara Shuzo) was used as the host of genetic manipulation. The aforementioned pXK4 was produced as follows. A shuttle vector pHK4 for coryneform bacteria and *Escherichia coli* (Japanese Patent Laid-open No. 5-7491/1993) was digested with restriction enzymes *Bam*HI and *Kpn*I to obtain a DNA fragment containing the replication origin, and the obtained fragment

was blunt-ended by using a DNA blunting kit (Blunting Kit produced by Takara Shuzo), ligated to an *Xba*I linker (produced by Takara Shuzo) and inserted into pHSG299 at the *Xba*I site to obtain the plasmid pKX4.

<2> Transfer of plasmid carrying *pdhA* gene into AJ12310 strain

[0167] The plasmid pPDHA-2 produced above was introduced into the *Corynebacterium thermoaminogenes* AJ12310 strain to prepare a *pdhA* gene-amplified strain. The transformation was performed in the same manner as Example 5, and a transformant was selected on CM-2B agar medium containing 25 µg/ml kanamycin to obtain AJ12310/pPDHA-2 strain.

<3> L-glutamic acid production by *pdhA*-amplified strain

[0168] The AJ12310 strain and the *pdhA* gene-amplified strain obtained above, AJ12310/pPDHA-2 strain, both of which were grown on CM-2B agar medium, were each inoculated to a 500-ml volume flask containing 20 ml of a medium for seed culture flask shown in Table 17, and cultured at 37°C with shaking until glucose was completely consumed. 2 ml of this culture broth was inoculated into 500 ml-volume flask containing 20 ml of a medium for main culture flask shown in Table 17, and cultured as main culture at 37°C and 44°C. The main culture was continued until glucose was completely consumed. After the culture, OD₆₂₀ of the medium and accumulated amount of L-glutamic acid were measured to examine the effect of the gene amplification on the cell formation and production of glutamic acid. The measurement of OD was performed by using a spectrophotometer HITACHI U-2000 (Hitachi), and L-glutamic acid concentration was measured by using a glutamic acid analyzer AS-210 (Asahi Chemical Industry). The results are shown in Fig. 18.

[0169] The *pdhA* gene-amplified strain, AJ12310/pPDHA-2 strain, showed increased L-glutamic acid accumulation and increased OD compared with the AJ12310 strain, and thus it became clear that the amplification of the *pdhA* gene was effective for L-glutamic acid production.

Table 17

| Medium for evaluation of <i>pdhA</i> -amplified strain | | |
|--|--------------|--------------|
| Medium composition | Seed culture | Main culture |
| Sucrose | 30 g/l | 60 g/l |
| KH ₂ PO ₄ | 1 g/l | 1 g/l |
| MgSO ₄ ·7H ₂ O | 0.4 g/l | 0.4 g/l |
| FeSO ₄ ·7H ₂ O | 0.01 g/l | 0.01 g/l |
| MnSO ₄ ·7H ₂ O | 0.01 g/l | 0.01 g/l |
| (NH ₄) ₂ SO ₄ | 15 g/l | 30 g/l |
| Soybean protein hydrolysate | 480 mg/l | 480 mg/l |
| Thiamin hydrochloride | 200 µg/l | 200 µg/l |
| Biotin | 10 µg/l | |
| AZ-20R (anti-foaming agent) | 20 µg/l | 20 µg/l |
| CaCO ₃ (separately sterilized) | 50 g/L | 50 g/L |
| pH 8.0 (adjusted with KOH) | | |

Example 7: L-glutamic acid production by *icd* gene-amplified strain

<1> Construction of plasmid pICD-4 carrying *icd* derived from *Corynebacterium thermoaminogenes* AJ12310 strain

[0170] Based on the *icd* gene sequence of the AJ12310 strain shown in SEQ ID NO: 29, the primers shown in SEQ ID NO: 103 and SEQ ID NO: 104 were synthesized. A *Bgl*II site was introduced into 5' end of the both primers. Separately, genomic DNA of the *Corynebacterium thermoaminogenes* AJ12310 strain was prepared by using a Genomic DNA Purif. Kit (Edge BioSystems). Sterilized water was added to the genome DNA as a template, 100 pmol each of the aforementioned primers, 8 µl of dNTP mixture (2.5 mM each), 10 µl of 10 x Pyrobest Buffer II (Takara Shuzo) and

2.5 U of Pyrobest polymerase (Takara Shuzo) to prepare a PCR reaction mixture in a total volume of 100 μ l. PCR was performed with a cycle of denaturation at 98°C for 10 seconds, association at 55°C for 1 minute and extension reaction at 72°C for 4 minutes, which was repeated for 30 cycles, by using the above reaction mixture and a thermal cycler TP240 (Takara Shuzo) to amplify a DNA fragment of about 3.3 kb containing the *icd* gene and its promoter.

[0171] Then, this DNA fragment containing the *icd* gene was digested with *Bgl*II, and ligated to pHSG299 (Takara Shuzo) at the *Bam*HI site. This plasmid was then treated with *Xba*I, and a fragment obtained by digesting pXK4 with *Xba*I was inserted into the plasmid to construct pICD-4. The construction procedure of pICD-4 is shown in Fig. 19. A DNA Ligation Kit Ver.2 (Takara Shuzo) was used for the ligation reaction, and *Escherichia coli* JM109 strain (Takara Shuzo) was used as the host of genetic manipulation.

<2> Transfer of plasmid carrying *icd* gene into AJ12310 strain

[0172] The plasmid pICD-4 produced above was introduced into the *Corynebacterium thermoaminogenes* AJ12310 strain to prepare an *icd* gene-amplified strain. The transformation was performed in the same manner as Example 5, and a transformant was selected on CM-2B agar medium containing 25 μ g/ml kanamycin to obtain AJ12310/pICD-4 strain.

<3> L-glutamic acid production by *icd*-amplified strain

[0173] Culture evaluation was performed for the AJ12310 strain and the *icd*-amplified strain thereof, AJ12310/pICD, by the culture method described in Example 6. The results are shown in Fig. 20. The *icd* gene-amplified strain AJ12310/pICD-4 strain showed increased L-glutamic acid accumulation and increased OD compared with the AJ12310 strain, and thus it became clear that the amplification of the *icd* gene was effective for L-glutamic acid production.

Example 8: L-glutamic acid production by *gdh* gene-amplified strain

<1> Construction of plasmid carrying *gdh* derived from *Corynebacterium thermoaminogenes* AJ12310 strain

[0174] Based on the *gdh* gene sequence of the AJ12310 strain shown in SEQ ID NO: 79, the primers shown in SEQ ID NO: 105 and SEQ ID NO: 106 were synthesized.

[0175] Separately, chromosomal DNA of the AJ12310 strain was prepared by using a Bacterial Genome DNA Purification Kit (Advanced Genetic Technologies Corp.). Sterilized water was added to 0.5 μ g of this chromosomal DNA, 10 pmol each of the aforementioned oligonucleotides, 8 μ l of dNTP mixture (2.5 mM each), 5 μ l of 10 x LA Taq Buffer (Takara Shuzo) and 2 U of LA Taq (Takara Shuzo) to prepare a PCR reaction mixture in a total volume of 50 μ l. PCR was performed with a cycle of denaturation at 94°C for 30 seconds, association at 55°C for 1 second and extension reaction at 72°C for 3 minutes, which was repeated for 30 cycles, by using the above reaction mixture and a thermal cycler TP240 (Takara Shuzo) to amplify a DNA fragment of about 2 kb containing the *gdh* gene and its promoter. The obtained amplified fragment was digested with *Pst*I (Takara Shuzo), mixed with pHSG299 (Takara Shuzo) fully digested with *Pst*I and ligated to it. A DNA Ligation Kit Ver.2 produced by Takara Shuzo was used for the ligation reaction. After the ligation, competent cells of *Escherichia coli* JM109 (produced by Takara Shuzo) were transformed with the ligation product, plated on L medium (10 g/l of Bacto-trypton, 5 g/l of Bacto-yeast extract, 5 g/l of NaCl, 15 g/l of agar, pH 7.2) containing 10 μ g/ml of IPTG (isopropyl- β -D-thiogalactopyranoside), 40 μ g/ml of X-Gal (5-bromo-4-chloro-3-indolyl- β -D-galactoside) and 40 μ g/ml of chloramphenicol, and cultured overnight. The emerged white colonies were picked up and subjected to single colony separation to obtain transformants.

[0176] Plasmids were prepared from the transformants by the alkali method (Text for Bioengineering Experiments, Edited by the Society for Bioscience and Bioengineering, Japan, p.105, Baifukan, 1992) and their restriction maps were prepared. A plasmid having a restriction map equivalent to that shown in Fig. 21 was designated as pHSG299YGDH.

[0177] A replication origin that functions in coryneform bacteria was introduced into this pHSG299YGDH. Specifically, pXC4 was digested with a restriction enzyme *Xba*I to obtain a fragment containing a replication origin derived from pHM1519, and it was mixed with pHSG299YGDH fully digested with *Xba*I and ligated to it. Plasmids were prepared in the same manner as above and a plasmid having a restriction map equivalent to that shown in Fig. 21 was designated as pYGDH. pXC4 was constructed in the same manner as that for pXK4 mentioned in Example 6 except that pHSG399 (Cm^r) was used instead of pHSG299.

<2> Transfer of plasmid carrying *gdh* gene into AJ12310

[0178] The plasmid produced above was introduced into the *Corynebacterium thermoaminogenes* AJ12310 strain

to prepare a *gdh* gene-amplified strain. The transformation was performed in the same manner as Example 5, and a transformant was selected on CM-2B agar medium containing 25 µg/ml kanamycin at 31°C to obtain AJ12310/pYGDH.

<3> L-glutamic acid production by *gdh*-amplified strain

[0179] The AJ12310 strain and the *gdh* gene-amplified strain obtained above, AJ12310/pYGDH strain, both of which were grown on CM-2B agar medium, were each inoculated to a 500-ml volume flask containing 20 ml of a medium for seed culture flask shown in Table 18, and cultured at 37°C with shaking until glucose was completely consumed. 2 ml of this culture broth was inoculated into 500 ml-volume flask containing 20 ml of a medium for main culture flask shown in Table 19, and cultured as main culture at 37°C and 44°C. The main culture was continued until glucose was completely consumed. After completion of the culture, OD₆₂₀ of the medium and accumulated amount of L-glutamic acid were measured to examine the effect of the gene amplification on the cell formation and production of glutamic acid. The measurement of OD was performed by using a spectrophotometer HITACHI U-2000 (Hitachi), and L-glutamic acid concentration was measured by using a glutamic acid analyzer AS-210 (Asahi Chemical Industry).

Table 18

| Composition of medium for seed culture | |
|---|---------------|
| Medium composition | Concentration |
| Glucose | 30 g/l |
| Ammonium sulfate | 15 g/l |
| KH ₂ PO ₄ | 1 g/l |
| MgSO ₄ ·7H ₂ O | 0.4 g/l |
| FeSO ₄ ·7H ₂ O | 0.01 g/l |
| MnSO ₄ ·7H ₂ O | 0.01 g/l |
| Soybean protein hydrolysate | 0.48 g/l |
| Thiamin hydrochloride | 200 µg/l |
| Biotin | 10 µg/l |
| AZ20R | 0.02 ml/l |
| CaCO ₃ (separately sterilized) | 1 g/L |
| pH 8.0 (adjusted with KOH) | |

Table 19

| Composition of medium for main culture | |
|---|---------------|
| Medium composition | Concentration |
| Glucose | 60 g/l |
| Ammonium sulfate | 30 g/l |
| KH ₂ PO ₄ | 1 g/l |
| MgSO ₄ ·7H ₂ O | 0.4 g/l |
| FeSO ₄ ·7H ₂ O | 0.01 g/l |
| MnSO ₄ ·7H ₂ O | 0.01 g/l |
| Soybean protein hydrolysate | 0.48 g/l |
| Thiamin hydrochloride | 200 µg/l |
| AZ20R | 0.02 ml/l |
| CaCO ₃ (separately sterilized) | 1 g/L |
| PH 8.0 (adjusted with KOH) | |

[0180] The results of the culture are shown in Table 20 and Table 21. At 37°C, the *gdh*-amplified strain showed higher saccharide consuming rate, better growth and higher attained OD compared with the parent strain, the AJ12310 strain. Moreover, both of the L-glutamic acid accumulation and the yield were markedly improved, i.e., 5-7% at 37°C. Also at 44°C, the yield was improved, and the attained OD increased. On the other hand, it was confirmed that accumulation of α -ketoglutaric acid was decreased in the *gdh*-amplified strain. These results demonstrate that the amplification of *gdh* is effective for improvement in L-glutamic acid yield and reduction of byproduct.

Table 20

| Culture result of <i>gdh</i> -amplified strain (37°C) | | | | |
|---|----------------------------|------------------------------|--------------------|-------------------------|
| | OD ₆₂₀ (51x) | L-Glu accumulation (g/dl) | L-Glu yield (%) | α -KG (mg/dl) |
| AJ12310 | 0.58 | 1.74 | 30.7 | 53.9 |
| AJ12310/PYGDH | 0.65 | 2.23 | 39.3 | 4.1 |

Table 21

| Culture result of <i>gdh</i> -amplified strain (44°C) | | | |
|---|----------------------------|------------------------------|--------------------|
| | OD ₆₂₀ (51x) | L-Glu accumulation (g/dl) | L-Glu yield (%) |
| AJ12310 | 0.63 | 1.70 | 26.7 |
| AJ12310/pYGDH | 0.71 | 1.79 | 27.8 |

Example 9: L-glutamic acid production by *gltA* gene-amplified strain

<1> Construction of plasmid carrying *gltA* gene derived from *Corynebacterium thermoaminogenes*

[0181] Based on the *gltA* gene sequence of the AJ12310 strain shown in SEQ ID NO: 89, the primers shown in SEQ ID NO: 107 and SEQ ID NO: 108 were synthesized.

[0182] Separately, chromosomal DNA of the AJ12310 strain was prepared by using a Bacterial Genome DNA Purification Kit (Advanced Genetic Technologies Corp.). Sterilized water was added to 0.5 μ g of this chromosomal DNA, 10 pmol each of the aforementioned oligonucleotides, 8 μ l of dNTP mixture (2.5 mM each), 10 μ l of 10 x Pyrobest-Taq Buffer (Takara Shuzo) and 2 U of Pyrobest Taq (Takara Shuzo) to prepare a PCR reaction mixture in a total volume of 100 μ l. PCR was performed with a cycle of denaturation at 94°C for 30 seconds, association at 45°C for 30 seconds and extension reaction at 72°C for 3 minutes, which was repeated for 30 cycles, by using the above reaction mixture and a thermal cycler TP240 (Takara Shuzo) to amplify a DNA fragment of about 2 kb containing the *gltA* gene and its promoter. The obtained amplified fragment was digested with *KpnI* (Takara Shuzo), mixed with pHSG299 (Takara Shuzo) fully digested with *KpnI* and ligated to it. A DNA Ligation Kit Ver.2 produced by Takara Shuzo was used for the ligation reaction. After the ligation, competent cells of *Escherichia coli* JM109 (produced by Takara Shuzo) were transformed with the ligation product, plated on L medium (10 g/l of Bacto-trypton, 5 g/l of Bacto-yeast extract, 5 g/l of NaCl, 15 g/l of agar, pH 7.2) containing 10 μ g/ml of IPTG (isopropyl- β -D-thiogalactopyranoside), 40 μ g/ml of X-Gal (5-bromo-4-chloro-3-indolyl- β -D-galactoside) and 40 μ g/ml of chloramphenicol, and cultured overnight. The emerged white colonies were picked up and subjected to single colony separation to obtain transformants.

[0183] Plasmids were prepared from the transformants by the alkali method (Text for Bioengineering Experiments, Edited by the Society for Bioscience and Bioengineering, Japan, p.105, Baifukan, 1992) and their restriction maps were prepared. A plasmid having a restriction map equivalent to that shown in Fig. 22 was designated as pHSG299YCS.

[0184] A replication origin that is replicable in coryneform bacteria was introduced into this pHSG299YCS. Specifically, pXC4 was digested with a restriction enzyme *XbaI* to obtain a fragment containing a replication origin derived from pHM1519, and it was mixed with pHSG299YCS fully digested with *XbaI* and ligated to it. Plasmids were prepared in the same manner as above and a plasmid having a restriction map equivalent to that shown in Fig. 22 was designated as pYCS.

<2> Transfer of plasmid carrying *gltA* gene into AJ12310 strain

[0185] The plasmid produced above was introduced into the *Corynebacterium thermoaminogenes* AJ12310 strain

to prepare a *gltA* gene-amplified strain. The transformation was performed in the same manner as Example 5, and a transformant was selected on CM-2B agar medium containing 25 µg/ml kanamycin to obtain AJ12310/pYCS.

<3> L-glutamic acid production by *gltA*-amplified strain

[0186] The AJ12310 strain and the *gltA* gene-amplified strain obtained above, AJ12310/pYCS strain, both of which were grown on CM-2B agar medium, were cultured in the same manner as in Example 8. The results of the culture are shown in Table 22 and Table 23. Both at the culture temperatures, 37°C and 44°C, the CS-enhanced strain showed improved glutamic acid accumulation compared with the parent strain. Further, the *gltA*-amplified strain showed decreased L-aspartic acid and L-lysine, which are synthesized from oxaloacetic acid.

[0187] These results demonstrate that the amplification of *gltA* is effective for improvement of L-glutamic acid yield and reduction of byproduct.

Table 22

| Culture result of <i>gltA</i> -amplified strain (37°C) | | | | |
|--|---------------------------|-----------|----------------------------|----------------------------|
| | L-Glu accumulation (g/dl) | Yield (%) | L-Asp accumulation (mg/dl) | L-Lys accumulation (mg/dl) |
| AJ12310 | 1.79 | 31.9 | 11.8 | 11.0 |
| AJ12310/pYCS | 2.04 | 36.5 | 8.1 | 7.3 |

Table 23

| Culture result of <i>gltA</i> -amplified strain (44°C) | | | | | |
|--|------|---------------------------|-----------|----------------------------|----------------------------|
| | OD | L-Glu accumulation (g/dl) | Yield (%) | L-Asp accumulation (mg/dl) | L-Lys Accumulation (mg/dl) |
| AJ12310 | 0.58 | 1.38 | 21.8 | 23.3 | 29.2 |
| AJ12310/pYCS | 0.65 | 1.84 | 28.8 | 14.1 | 17.2 |

[Explanation of Sequence Listing]

[0188]

SEQ ID NO: 1: *aceA*, nucleotide sequence
 SEQ ID NO: 2: *aceA*, amino acid sequence
 SEQ ID NO: 3: *accBC*, nucleotide sequence
 SEQ ID NO: 4: *accBC*, amino acid sequence
 SEQ ID NO: 5: *dtSR1*, nucleotide sequence
 SEQ ID NO: 6: *dtSR1*, amino acid sequence
 SEQ ID NO: 7: *dtSR2*, nucleotide sequence
 SEQ ID NO: 8: *dtSR2*, amino acid sequence
 SEQ ID NO: 9: *pfk*, nucleotide sequence
 SEQ ID NO: 10: *pfk*, amino acid sequence
 SEQ ID NO: 11: *scrB* (AJ12340), nucleotide sequence
 SEQ ID NO: 12: *scrB* (AJ12340), amino acid sequence
 SEQ ID NO: 13: *scrB* (AJ12309), nucleotide sequence
 SEQ ID NO: 14: *scrB* (AJ12309), amino acid sequence
 SEQ ID NO: 15: *scrB* (AJ12310), nucleotide sequence
 SEQ ID NO: 16: *gluABCD*, nucleotide sequence
 SEQ ID NO: 17: *gluABCD*, amino acid sequence
 SEQ ID NO: 18: *gluABCD*, amino acid sequence
 SEQ ID NO: 19: *gluABCD*, amino acid sequence
 SEQ ID NO: 20: *gluABCD*, amino acid sequence
 SEQ ID NO: 21: *pdhA*, nucleotide sequence
 SEQ ID NO: 22: *pdhA*, amino acid sequence

SEQ ID NO: 23: *pc*, nucleotide sequence
SEQ ID NO: 24: *pc*, amino acid sequence
SEQ ID NO: 25: *ppc*, nucleotide sequence
SEQ ID NO: 26: *ppc*, amino acid sequence
5 SEQ ID NO: 27: *acn*, nucleotide sequence
SEQ ID NO: 28: *acn*, amino acid sequence
SEQ ID NO: 29: *icd*, nucleotide sequence
SEQ ID NO: 30: *icd*, amino acid sequence
SEQ ID NO: 31: *lpd*, nucleotide sequence
10 SEQ ID NO: 32: *lpd*, amino acid sequence
SEQ ID NO: 33: *odhA*, nucleotide sequence
SEQ ID NO: 34: *odhA*, amino acid sequence
SEQ ID NO: 79: *gdh* (AJ12310), nucleotide sequence
SEQ ID NO: 80: *gdh* (AJ12310), amino acid sequence
15 SEQ ID NO: 81: *gdh* (2256), nucleotide sequence
SEQ ID NO: 82: *gdh* (2256), amino acid sequence
SEQ ID NO: 89: *gltA* (AJ12310), nucleotide sequence
SEQ ID NO: 90: *gltA* (AJ12310), amino acid sequence
SEQ ID NO: 91: *gltA* (2256), nucleotide sequence
20 SEQ ID NO: 92: *gltA* (2256), amino acid sequence
SEQ ID NO: 93: *scrB* (AJ12309), nucleotide sequence
SEQ ID NO: 94: *scrB* (AJ12309), amino acid sequence

Industrial Applicability

25 [0189] According to the present invention, genes coding for enzymes of amino acid biosynthetic pathway derived from *Corynebacterium thermoaminogenes*, or genes coding for proteins involved in the amino acid uptake into cells.

[0190] The genes of the present invention can be utilized for the production of the aforementioned enzymes or proteins, or the breeding of amino acid producing bacteria.

SEQUENCE LISTING

<110> Ajinomoto Co., Inc.

<120> Genes for Heat resistant Enzymes of Amino Acid
Biosynthetic Pathway Derived from Thermophilic
Coryneform Bacteria

<130> EPA-53881

<140>

<141> 10.04.2002

<150> JP 11-282716

<151> 1999-10-04

<150> JP 11-311147

<151> 1999-11-01

<150> JP 2000-120687

<151> 2000-04-21

<160> 108

<170> PatentIn Ver. 2.0

<210> 1

<211> 1980

<212> DNA

<213> Corynebacterium thermoaminogenes

<220>

<221> CDS

<222> (577)..(1869)

<400> 1

```

tgcatlccac cgacggcac gcgttcggc tigtacgcg cgtaalcg ctgatggc 60
atgcaaagc ccttcgaagc aagagatcg gigtgicg gcacclac ggggaagcc 120
tcgctgcgc ccagggggag cggcgagc gaccaggta agigataacc atcacctgc 180
caatgggill gcgaactlla ccgigacgc accccgcil tglitgatc acaccagc 240
gaaggctgc gcttttcga agatgcacg gaagtggca alecttgcca cccgaggt 300
tcccaglaca aacglactag tgalgaggat cacggggaac attgiggaga tgcacillg 360

```


caatatttgc aaaaggggig actacccccg cgcaaaacti aaaaacccaa atccgttgac 420
 ggaccaatgc ccgatgaagc aatgltgaa gcacgccacc ggaacacagg ttgttgatca 480
 5 ctcaccaatga tgtgggggat tgcatacaca cagtgtgcag ggcggcacct ctaccgaatg 540
 cgccttacag cagcaccaag aagaagtgac tcttag atg tca aac gtt gga acg 594
 Met Ser Asn Val Gly Thr
 1 5
 10 cca cgt acc gca cag gaa atc cag cag gat tgg gac acc aac cca cgc 642
 Pro Arg Thr Ala Gln Glu Ile Gln Gln Asp Trp Asp Thr Asn Pro Arg
 10 15 20
 15 tgg aac gga atc acc cgc gac tac acc gct gag cag gla gct gag ctc 690
 Trp Asn Gly Ile Thr Arg Asp Tyr Thr Ala Glu Gln Val Ala Glu Leu
 25 30 35
 cag ggc agc gtc gtc gag gag cac acc ctc gca aag cgc ggc gcc gag 738
 Gln Gly Ser Val Val Glu Glu His Thr Leu Ala Lys Arg Gly Ala Glu
 40 45 50
 20 atc ctg tgg gat gca gtt tcc gca gag ggc gac gac tac atc aac gca 786
 Ile Leu Trp Asp Ala Val Ser Ala Glu Gly Asp Asp Tyr Ile Asn Ala
 55 60 65 70
 25 ctg ggc gcc ctt acc ggt aac cag gct gtc cag cag gtc cgt gcc ggc 834
 Leu Gly Ala Leu Thr Gly Asn Gln Ala Val Gln Gln Val Arg Ala Gly
 75 80 85
 30 ctg aag gct gtc tac ctc tcc ggc tgg cag gtc gca ggt gac gcc aac 882
 Leu Lys Ala Val Tyr Leu Ser Gly Trp Gln Val Ala Gly Asp Ala Asn
 90 95 100
 ctc gcc ggt cac acc tac ccc gac cag tcc ctg tac ccg gcg aac tcc 930
 Leu Ala Gly His Thr Tyr Pro Asp Gln Ser Leu Tyr Pro Ala Asn Ser
 105 110 115
 35 gtc ccg aac gtt gtc cgt cgc atc aac aac gca ctg ctg cgc gcc gat 978
 Val Pro Asn Val Val Arg Arg Ile Asn Asn Ala Leu Leu Arg Ala Asp
 120 125 130
 40 gag atc gca cgc gtc gag ggt gac acc tcc gtc gac aac tgg ctg gtc 1026
 Glu Ile Ala Arg Val Glu Gly Asp Thr Ser Val Asp Asn Trp Leu Val
 135 140 145 150
 45 ccg atc gtc gcc gac ggc gag gcc ggc ttc ggt ggc gcc ctc aac gtc 1074
 Pro Ile Val Ala Asp Gly Glu Ala Gly Phe Gly Gly Ala Leu Asn Val
 155 160 165
 lac gag ctg cag aag ggc atg atc acc gct ggt gcc gca ggc acc cac 1122
 Tyr Glu Leu Gln Lys Gly Met Ile Thr Ala Gly Ala Ala Gly Thr His
 170 175 180
 50 tgg gag gat cag ctg gct tcc gag aag aag tgt ggc cac ctg ggt ggc 1170
 Trp Glu Asp Gln Leu Ala Ser Glu Lys Lys Cys Gly His Leu Gly Gly
 185 190 195
 55 aag gtc ctg atc ccg acc cag cag cac atc cgc acc ctg aac tcc gcc 1218

| | Lys | Val | Leu | Ile | Pro | Thr | Gln | Gln | His | Ile | Arg | Thr | Leu | Asn | Ser | Ala | |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------------|-----------|-----|-----|-----|-----|-----|------|
| | 200 | | | | | | 205 | | | | | 210 | | | | | |
| 5 | cgc | ctg | gca | gct | gac | gtg | gcc | aac | acc | ccg | acc | gtc | gtc | atc | gcc | cgc | 1266 |
| | Arg | Leu | Ala | Ala | Asp | Val | Ala | Asn | Thr | Pro | Thr | Val | Val | Ile | Ala | Arg | |
| | 215 | | | | | 220 | | | | 225 | | | | | 230 | | |
| 10 | acc | gac | gca | gag | gcc | gcc | acc | ctg | atc | acc | tct | gat | glt | gat | gag | cgc | 1314 |
| | Thr | Asp | Ala | Glu | Ala | Ala | Thr | Leu | Ile | Thr | Ser | Asp | Val | Asp | Glu | Arg | |
| | | | | | 235 | | | | | 240 | | | | 245 | | | |
| | gac | cgc | cca | ttc | atc | acc | ggc | gag | cgc | acc | gcc | gag | ggc | tac | tac | cac | 1362 |
| | Asp | Arg | Pro | Phe | Ile | Thr | Gly | Glu | Arg | Thr | Ala | Glu | Gly | Tyr | Tyr | His | |
| 15 | | | 250 | | | | | 255 | | | | | | 260 | | | |
| | gtc | aag | ccg | ggt | ctc | gag | ccc | tgc | atc | gca | cgt | gcg | aag | tcc | tac | gct | 1410 |
| | Val | Lys | Pro | Gly | Leu | Glu | Pro | Cys | Ile | Ala | Arg | Ala | Lys | Ser | Tyr | Ala | |
| | | | 265 | | | | | 270 | | | | | | 275 | | | |
| 20 | ccc | tac | gca | gac | atg | atc | tgg | atg | gag | acc | ggc | acc | ccf | gac | ctc | gag | 1458 |
| | Pro | Tyr | Ala | Asp | Met | Ile | Trp | Met | Glu | Thr | Gly | Thr | Pro | Asp | Leu | Glu | |
| | | | 280 | | | | 285 | | | | | 290 | | | | | |
| | ctg | gcc | aag | aag | ttc | gcc | gag | ggc | gtc | cgc | agc | gag | ttc | ccg | gac | cag | 1506 |
| 25 | Leu | Ala | Lys | Lys | Phe | Ala | Glu | Gly | Val | Arg | Ser | Glu | Phe | Pro | Asp | Gln | |
| | 295 | | | | 300 | | | | | 305 | | | | | 310 | | |
| | ctg | ctg | tcc | tac | aac | tgc | tcc | ccg | tcc | ttc | aac | tgg | tct | gca | cac | ctc | 1554 |
| | Leu | Leu | Ser | Tyr | Asn | Cys | Ser | Pro | Ser | Phe | Asn | Trp | Ser | Ala | His | Leu | |
| 30 | | | | | 315 | | | | | 320 | | | | 325 | | | |
| | gag | gcc | gac | gag | atc | gct | aag | ttc | cag | aag | gaa | ctg | ggt | gcc | atg | ggc | 1602 |
| | Glu | Ala | Asp | Glu | Ile | Ala | Lys | Phe | Gln | Lys | Glu | Leu | Gly | Ala | Met | Gly | |
| | | | 330 | | | | | 335 | | | | 340 | | | | | |
| 35 | ttc | aag | ttc | cag | ttc | atc | acc | ctg | gct | ggc | ttc | cac | tcc | ctc | aac | tac | 1650 |
| | Phe | Lys | Phe | Gln | Phe | Ile | Thr | Leu | Ala | Gly | Phe | His | Ser | Leu | Asn | Tyr | |
| | | | 345 | | | | | 350 | | | | 355 | | | | | |
| | ggt | atg | ttc | gac | ctg | gct | tac | ggc | tac | gcc | cgt | gaa | ggc | atg | ccc | gcc | 1698 |
| 40 | Gly | Met | Phe | Asp | Leu | Ala | Tyr | Gly | Tyr | Ala | Arg | Glu | Gly | Met | Pro | Ala | |
| | | | 360 | | | | 365 | | | | | 370 | | | | | |
| | ttc | gtc | gac | ctg | cag | aac | cgt | gag | ttc | aag | gca | gct | gag | gag | cgc | ggc | 1746 |
| | Phe | Val | Asp | Leu | Gln | Asn | Arg | Glu | Phe | Lys | Ala | Ala | Glu | Glu | Arg | Gly | |
| 45 | 375 | | | | 380 | | | | | 385 | | | | | 390 | | |
| | ttc | acc | gcc | gtc | aag | cac | cag | cgt | gag | gtc | ggc | gcc | ggc | tac | ttc | gac | 1794 |
| | Phe | Thr | Ala | Val | Lys | His | Gln | Arg | Glu | Val | Gly | Ala | Gly | Tyr | Phe | Asp | |
| | | | | | 395 | | | | 400 | | | | 405 | | | | |
| 50 | acc | atc | gcc | acc | acc | gtt | gac | ccg | aac | tcc | tcc | acc | acc | gcg | ctg | aag | 1842 |
| | Thr | Ile | Ala | Thr | Thr | Val | Asp | Pro | Asn | Ser | Ser | Thr | Thr | Ala | Leu | Lys | |
| | | | 410 | | | | | 415 | | | | 420 | | | | | |
| | ggt | tcc | acc | gag | gaa | tgc | cag | ttc | cac | taggaaccac | ctgatgcgt | | | | | | 1889 |
| 55 | Gly | Ser | Thr | Glu | Glu | Cys | Gln | Phe | His | | | | | | | | |

425

430

gccgtatggc ctagcggcac cgcctctccc ttgcactcc agtactcctt tgtgcacatc 1949
 ggccatctcc acaccgcgcg ccccgccacc t 1980

<210> 2

<211> 431

<212> PRT

<213> Corynebacterium thermoaminogenes

<400> 2

15 Met Ser Asn Val Gly Thr Pro Arg Thr Ala Gln Glu Ile Gln Gln Asp
 1 5 10 15
 Trp Asp Thr Asn Pro Arg Trp Asn Gly Ile Thr Arg Asp Tyr Thr Ala
 20 25 30
 Glu Gln Val Ala Glu Leu Gln Gly Ser Val Val Glu Glu His Thr Leu
 35 40 45
 Ala Lys Arg Gly Ala Glu Ile Leu Trp Asp Ala Val Ser Ala Glu Gly
 50 55 60
 25 Asp Asp Tyr Ile Asn Ala Leu Gly Ala Leu Thr Gly Asn Gln Ala Val
 65 70 75 80
 Gln Gln Val Arg Ala Gly Leu Lys Ala Val Tyr Leu Ser Gly Trp Gln
 85 90 95
 30 Val Ala Gly Asp Ala Asn Leu Ala Gly His Thr Tyr Pro Asp Gln Ser
 100 105 110
 Leu Tyr Pro Ala Asn Ser Val Pro Asn Val Val Arg Arg Ile Asn Asn
 115 120 125
 35 Ala Leu Leu Arg Ala Asp Glu Ile Ala Arg Val Glu Gly Asp Thr Ser
 130 135 140
 Val Asp Asn Trp Leu Val Pro Ile Val Ala Asp Gly Glu Ala Gly Phe
 145 150 155 160
 40 Gly Gly Ala Leu Asn Val Tyr Glu Leu Gln Lys Gly Met Ile Thr Ala
 165 170 175
 Gly Ala Ala Gly Thr His Trp Glu Asp Gln Leu Ala Ser Glu Lys Lys
 180 185 190
 45 Cys Gly His Leu Gly Gly Lys Val Leu Ile Pro Thr Gln Gln His Ile
 195 200 205
 Arg Thr Leu Asn Ser Ala Arg Leu Ala Ala Asp Val Ala Asn Thr Pro
 210 215 220
 50 Thr Val Val Ile Ala Arg Thr Asp Ala Glu Ala Ala Thr Leu Ile Thr
 225 230 235 240
 Ser Asp Val Asp Glu Arg Asp Arg Pro Phe Ile Thr Gly Glu Arg Thr
 245 250 255
 55 Ala Glu Gly Tyr Tyr His Val Lys Pro Gly Leu Glu Pro Cys Ile Ala

260 265 270
 Arg Ala Lys Ser Tyr Ala Pro Tyr Ala Asp Met Ile Trp Met Glu Thr
 275 280 285
 Gly Thr Pro Asp Leu Glu Leu Ala Lys Lys Phe Ala Glu Gly Val Arg
 290 295 300
 Ser Glu Phe Pro Asp Gln Leu Leu Ser Tyr Asn Cys Ser Pro Ser Phe
 305 310 315 320
 Asn Trp Ser Ala His Leu Glu Ala Asp Glu Ile Ala Lys Phe Gln Lys
 325 330 335
 Glu Leu Gly Ala Met Gly Phe Lys Phe Gln Phe Ile Thr Leu Ala Gly
 340 345 350
 Phe His Ser Leu Asn Tyr Gly Met Phe Asp Leu Ala Tyr Gly Tyr Ala
 355 360 365
 Arg Glu Gly Met Pro Ala Phe Val Asp Leu Gln Asn Arg Glu Phe Lys
 370 375 380
 Ala Ala Glu Glu Arg Gly Phe Thr Ala Val Lys His Gln Arg Glu Val
 385 390 395 400
 Gly Ala Gly Tyr Phe Asp Thr Ile Ala Thr Thr Val Asp Pro Asn Ser
 405 410 415
 Ser Thr Thr Ala Leu Lys Gly Ser Thr Glu Glu Cys Gln Phe His
 420 425 430

<210> 3

<211> 2381

<212> DNA

<213> *Corynebacterium thermoaminogenes*

<220>

<221> CDS

<222> (577).. (2349)

<400> 3

agcaggccgt gtgccaac ggcaacttc gcagccgcaa ggagatcgag gagggttact 60
 cgcacctcaa cctgccgag gacaccgagg tglactgccg cgtgggtgac cgcgcggccc 120
 acaccgggtt cgtgtgaag taccgtcagg gglttgaata cgtccgcaac tatgacgggt 180
 cctgggtcga gggggcaac algtgacgca tgcctatcgt ccagggtgat gagccgggct 240
 cactctagtc accccggggt caccctcccg gtcaccccg taccctcccg ggtacacccc 300
 ggggacgggg tglgaccagg atctccctg catgtggaca ccgggaaact ttgcttgga 360
 aatgaccalc cagtaccgta atgcgggat gtttaacgcg tccacagggt caccagaalc 420
 cggatcgtct aaccccccta ggggattcg ctaaaagat accgagttag tgtgaagaa 480
 taatgtgat cgcaggggca ctgcatatg ctgtatgca gtcaatgaac agtgcgggtc 540
 tctgtcgtga agaaaatcaa aaccaggagg gtttta gtc tca gtc gag acc agg 594

Val Ser Val Glu Thr Arg

5
 aag atc acc aag gta ctt gtc gcc aac cgt ggt gaa atc gca atc cgt 642
 Lys Ile Thr Lys Val Leu Val Ala Asn Arg Gly Glu Ile Ala Ile Arg
 10 15 20
 gtt ttc cgc gca gca cgg gat gaa ggc atc gcc tct gtc gcc gtc tac 690
 Val Phe Arg Ala Ala Arg Asp Glu Gly Ile Ala Ser Val Ala Val Tyr
 25 30 35
 10 gcg gag ccg gac gca gat gcc cct ttc gtc gag tat gcc gat gag gcc 738
 Ala Glu Pro Asp Ala Asp Ala Pro Phe Val Glu Tyr Ala Asp Glu Ala
 40 45 50
 15 ttc gca ctc ggt ggc cag act tcc gca gag tcc tac ctc gtc att gac 786
 Phe Ala Leu Gly Gly Gln Thr Ser Ala Glu Ser Tyr Leu Val Ile Asp
 55 60 65 70
 aag atc att gac gca gca cgc aag tcc ggt gca gac gct gtc cac ccc 834
 20 Lys Ile Ile Asp Ala Ala Arg Lys Ser Gly Ala Asp Ala Val His Pro
 75 80 85
 ggc tac ggc ttc ctc gcc gag aac gcc gat ttc gct gaa gct gtc atc 882
 Gly Tyr Gly Phe Leu Ala Glu Asn Ala Asp Phe Ala Glu Ala Val Ile
 25 90 95 100
 aac gag ggc ctg atc tgg atc gga cca tcc cct gag tcc atc cgt tcc 930
 Asn Glu Gly Leu Ile Trp Ile Gly Pro Ser Pro Glu Ser Ile Arg Ser
 105 110 115
 30 ctc ggt gac aag gtc acc gca cgc cac atc gcc aac aac gcc aac gca 978
 Leu Gly Asp Lys Val Thr Ala Arg His Ile Ala Asn Asn Ala Asn Ala
 120 125 130
 ccg atg gca ccg ggc acc aag gag cct gtc aag gac gcc gct gag gtt 1026
 35 Pro Met Ala Pro Gly Thr Lys Glu Pro Val Lys Asp Ala Ala Glu Val
 135 140 145 150
 gtc gcc ttc gcc gag gag ttc ggt ctc ccc atc gcc atc aag gct gcc 1074
 Val Ala Phe Ala Glu Glu Phe Gly Leu Pro Ile Ala Ile Lys Ala Ala
 40 155 160 165
 ttc ggt ggc ggc gga cgt ggc atg aag gtc gcc tac gag atg gac gag 1122
 Phe Gly Gly Gly Gly Arg Gly Met Lys Val Ala Tyr Glu Met Asp Glu
 170 175 180
 45 gtc gcc gac ctc ttc gaa tcc gcc acc cgt gag gcc acc gcc gcc ttc 1170
 Val Ala Asp Leu Phe Glu Ser Ala Thr Arg Glu Ala Thr Ala Ala Phe
 185 190 195
 ggt cgt ggt gag tgc ttc gtg gag cgc tac ctg gac aag gcc cgc cac 1218
 50 Gly Arg Gly Glu Cys Phe Val Glu Arg Tyr Leu Asp Lys Ala Arg His
 200 205 210
 gtc gag gca cag gtc atc gcc gac aag cac ggc aac gtt gtg gtc gcc 1266
 55 Val Glu Ala Gln Val Ile Ala Asp Lys His Gly Asn Val Val Val Ala
 215 220 225 230

| | | |
|----|---|------|
| | ggt acc cgt gac tgc tcc ctg cag cgt cgt ttc cag aag ctc gtc gag | 1314 |
| | Gly Thr Arg Asp Cys Ser Leu Gln Arg Arg Phe Gln Lys Leu Val Glu | |
| | 235 240 245 | |
| 5 | gag gca ccg gca ccg ttc ctc acc gat gag cag cgt gac cgc atc cac | 1362 |
| | Glu Ala Pro Ala Pro Phe Leu Thr Asp Glu Gln Arg Asp Arg Ile His | |
| | 250 255 260 | |
| 10 | ttc tcc gcc aag gct atc tgc cgc gag gcc ggt tac tac ggt gcc ggc | 1410 |
| | Ser Ser Ala Lys Ala Ile Cys Arg Glu Ala Gly Tyr Tyr Gly Ala Gly | |
| | 265 270 275 | |
| 15 | acc gtg gag tac ctg gtc ggt tcc gac gga ctg atc tcc ttc ctg gag | 1458 |
| | Thr Val Glu Tyr Leu Val Gly Ser Asp Gly Leu Ile Ser Phe Leu Glu | |
| | 280 285 290 | |
| | gtc aac acc cgc ctg cag gtg gag cac ccc gtc acc gag gag acc acc | 1506 |
| | Val Asn Thr Arg Leu Gln Val Glu His Pro Val Thr Glu Glu Thr Thr | |
| 20 | 295 300 305 310 | |
| | ggc atc gac ctg gtc cgc gag atg ttc cgc atc gcc gag ggc gcc gag | 1554 |
| | Gly Ile Asp Leu Val Arg Glu Met Phe Arg Ile Ala Glu Gly Ala Glu | |
| | 315 320 325 | |
| 25 | ctc tcc atc aag gag gac ccg acc cca cgc ggc cac gcc ttc gag ttc | 1602 |
| | Leu Ser Ile Lys Glu Asp Pro Thr Pro Arg Gly His Ala Phe Glu Phe | |
| | 330 335 340 | |
| | cgc atc aac ggc gag gac gca ggc tcc aac ttc atg ccc gca ccg ggc | 1650 |
| 30 | Arg Ile Asn Gly Glu Asp Ala Gly Ser Asn Phe Met Pro Ala Pro Gly | |
| | 345 350 355 | |
| | aag atc acc cgc tac cgt gag ccc gcc ggc ccg ggt gtc cgc atg gac | 1698 |
| | Lys Ile Thr Arg Tyr Arg Glu Pro Ala Gly Pro Gly Val Arg Met Asp | |
| 35 | 360 365 370 | |
| | ttc ggc gtt gtc gag ggt tcc gag atc tcc ggc cag ttc gac tcc atg | 1746 |
| | Ser Gly Val Val Glu Gly Ser Glu Ile Ser Gly Gln Phe Asp Ser Met | |
| | 375 380 385 390 | |
| 40 | ctg gcc aag ctg atc gtc tgg ggc cag acc cgt gag cag gcc ctg gag | 1794 |
| | Leu Ala Lys Leu Ile Val Trp Gly Gln Thr Arg Glu Gln Ala Leu Glu | |
| | 395 400 405 | |
| | cgt tcc cgt cgt ggc ctc ggc gag tac atc gtc gag ggc atg ccg acc | 1842 |
| 45 | Arg Ser Arg Arg Ala Leu Gly Glu Tyr Ile Val Glu Gly Met Pro Thr | |
| | 410 415 420 | |
| | gtc atc ccg ttc cac tcc cac atc gtc tcc aac ccg gca ttc gtc ggt | 1890 |
| | Val Ile Pro Phe His Ser His Ile Val Ser Asn Pro Ala Phe Val Gly | |
| 50 | 425 430 435 | |
| | gac ggc gag ggc ttc gag gtc tac acc aag tgg atc gag gag gtc tgg | 1938 |
| | Asp Gly Glu Gly Phe Glu Val Tyr Thr Lys Trp Ile Glu Glu Val Trp | |
| | 440 445 450 | |
| 55 | gac aac ccg atc gag ccg ttc gtc gat gca gcc gac ctc gac gac gag | 1986 |

Asp Asn Pro Ile Glu Pro Phe Val Asp Ala Ala Asp Leu Asp Asp Glu
 455 460 465 470
 5 gag aag acc ccg tcc cag aag gtc atc gtc gag atc gac ggc cgc cgc 2034
 Glu Lys Thr Pro Ser Gln Lys Val Ile Val Glu Ile Asp Gly Arg Arg
 475 480 485
 10 gtc gag gtc gct ctc ccg ggc gac ctc gct ctc ggc ggt ggc gca ggt 2082
 Val Glu Val Ala Leu Pro Gly Asp Leu Ala Leu Gly Gly Gly Ala Gly
 490 495 500
 gcc gcc aag aag aag ccg aag aag cgt cgc gca ggt ggc gcc aag gcc 2130
 Ala Ala Lys Lys Lys Pro Lys Lys Arg Arg Ala Gly Gly Ala Lys Ala
 15 505 510 515
 ggt gtc tcc ggt gac tcc gtc gca gcc ccg atg cag ggc acc gtc atc 2178
 Gly Val Ser Gly Asp Ser Val Ala Ala Pro Met Gln Gly Thr Val Ile
 520 525 530
 20 aag gtc aac gtt gag gac ggc gcc gag gtc tcc gag ggt gac acc gtc 2226
 Lys Val Asn Val Glu Asp Gly Ala Glu Val Ser Glu Gly Asp Thr Val
 535 540 545 550
 25 gtc gtt ctc gag gcc atg aag atg gag aac ccg gtc aag gcc cac aag 2274
 Val Val Leu Glu Ala Met Lys Met Glu Asn Pro Val Lys Ala His Lys
 555 560 565
 tcc ggt acc gtc tcc ggt ctg acc atc gcc gcg ggt gag ggc gtc acc 2322
 Ser Gly Thr Val Ser Gly Leu Thr Ile Ala Ala Gly Glu Gly Val Thr
 30 570 575 580
 aag ggt cag gtt ctc ctg gag atc aag taatcccttc aggggaacaga 2369
 Lys Gly Gln Val Leu Leu Glu Ile Lys
 585 590
 35 cagccctgtt ct 2381
 <210> 4
 <211> 591
 40 <212> PRT
 <213> Corynebacterium thermoaminogenes
 <400> 4
 45 Val Ser Val Glu Thr Arg Lys Ile Thr Lys Val Leu Val Ala Asn Arg
 1 5 10 15
 Gly Glu Ile Ala Ile Arg Val Phe Arg Ala Ala Arg Asp Glu Gly Ile
 20 25 30
 50 Ala Ser Val Ala Val Tyr Ala Glu Pro Asp Ala Asp Ala Pro Phe Val
 35 40 45
 Glu Tyr Ala Asp Glu Ala Phe Ala Leu Gly Gly Gln Thr Ser Ala Glu
 50 55 60
 55 Ser Tyr Leu Val Ile Asp Lys Ile Ile Asp Ala Ala Arg Lys Ser Gly

| | | | | | | | |
|----|-----|-----|-----|-----|-----|-----|---|
| | 65 | | 70 | | 75 | | 80 |
| | Ala | Asp | Ala | Val | His | Pro | Gly Tyr Gly Phe Leu Ala Glu Asn Ala Asp |
| | | | 85 | | | 90 | 95 |
| 5 | Phe | Ala | Glu | Ala | Val | Ile | Asn Glu Gly Leu Ile Trp Ile Gly Pro Ser |
| | | | 100 | | | 105 | 110 |
| | Pro | Glu | Ser | Ile | Arg | Ser | Leu Gly Asp Lys Val Thr Ala Arg His Ile |
| | | | 115 | | | 120 | 125 |
| 10 | Ala | Asn | Asn | Ala | Asn | Ala | Pro Met Ala Pro Gly Thr Lys Glu Pro Val |
| | | | 130 | | | 135 | 140 |
| | Lys | Asp | Ala | Ala | Glu | Val | Val Ala Phe Ala Glu Glu Phe Gly Leu Pro |
| | 145 | | | | 150 | | 155 160 |
| 15 | Ile | Ala | Ile | Lys | Ala | Ala | Phe Gly Gly Gly Arg Gly Met Lys Val |
| | | | 165 | | | 170 | 175 |
| | Ala | Tyr | Glu | Met | Asp | Glu | Val Ala Asp Leu Phe Glu Ser Ala Thr Arg |
| | | | 180 | | | 185 | 190 |
| 20 | Glu | Ala | Thr | Ala | Ala | Phe | Gly Arg Gly Glu Cys Phe Val Glu Arg Tyr |
| | | | 195 | | | 200 | 205 |
| | Leu | Asp | Lys | Ala | Arg | His | Val Glu Ala Gln Val Ile Ala Asp Lys His |
| | | | 210 | | | 215 | 220 |
| 25 | Gly | Asn | Val | Val | Val | Ala | Gly Thr Arg Asp Cys Ser Leu Gln Arg Arg |
| | 225 | | | | 230 | | 235 240 |
| | Phe | Gln | Lys | Leu | Val | Glu | Glu Ala Pro Ala Pro Phe Leu Thr Asp Glu |
| | | | 245 | | | 250 | 255 |
| 30 | Gln | Arg | Asp | Arg | Ile | His | Ser Ser Ala Lys Ala Ile Cys Arg Glu Ala |
| | | | 260 | | | 265 | 270 |
| | Gly | Tyr | Tyr | Gly | Ala | Gly | Thr Val Glu Tyr Leu Val Gly Ser Asp Gly |
| | | | 275 | | | 280 | 285 |
| 35 | Leu | Ile | Ser | Phe | Leu | Glu | Val Asn Thr Arg Leu Gln Val Glu His Pro |
| | | | 290 | | | 295 | 300 |
| | Val | Thr | Glu | Glu | Thr | Thr | Gly Ile Asp Leu Val Arg Glu Met Phe Arg |
| | 305 | | | | 310 | | 315 320 |
| 40 | Ile | Ala | Glu | Gly | Ala | Glu | Leu Ser Ile Lys Glu Asp Pro Thr Pro Arg |
| | | | 325 | | | 330 | 335 |
| | Gly | His | Ala | Phe | Glu | Phe | Arg Ile Asn Gly Glu Asp Ala Gly Ser Asn |
| | | | 340 | | | 345 | 350 |
| 45 | Phe | Met | Pro | Ala | Pro | Gly | Lys Ile Thr Arg Tyr Arg Glu Pro Ala Gly |
| | | | 355 | | | 360 | 365 |
| | Pro | Gly | Val | Arg | Met | Asp | Ser Gly Val Val Glu Gly Ser Glu Ile Ser |
| | | | 370 | | | 375 | 380 |
| 50 | Gly | Gln | Phe | Asp | Ser | Met | Leu Ala Lys Leu Ile Val Trp Gly Gln Thr |
| | 385 | | | | 390 | | 395 400 |
| | Arg | Glu | Gln | Ala | Leu | Glu | Arg Ser Arg Arg Ala Leu Gly Glu Tyr Ile |
| 55 | | | | | 405 | | 410 415 |

Val Glu Gly Met Pro Thr Val Ile Pro Phe His Ser His Ile Val Ser
 420 425 430
 5 Asn Pro Ala Phe Val Gly Asp Gly Glu Gly Phe Glu Val Tyr Thr Lys
 435 440 445
 Trp Ile Glu Glu Val Trp Asp Asn Pro Ile Glu Pro Phe Val Asp Ala
 450 455 460
 10 Ala Asp Leu Asp Asp Glu Glu Lys Thr Pro Ser Gln Lys Val Ile Val
 465 470 475 480
 Glu Ile Asp Gly Arg Arg Val Glu Val Ala Leu Pro Gly Asp Leu Ala
 485 490 495
 15 Leu Gly Gly Gly Ala Gly Ala Ala Lys Lys Lys Pro Lys Lys Arg Arg
 500 505 510
 Ala Gly Gly Ala Lys Ala Gly Val Ser Gly Asp Ser Val Ala Ala Pro
 515 520 525
 20 Met Gln Gly Thr Val Ile Lys Val Asn Val Glu Asp Gly Ala Glu Val
 530 535 540
 Ser Glu Gly Asp Thr Val Val Val Leu Glu Ala Met Lys Met Glu Asn
 545 550 555 560
 25 Pro Val Lys Ala His Lys Ser Gly Thr Val Ser Gly Leu Thr Ile Ala
 565 570 575
 Ala Gly Glu Gly Val Thr Lys Gly Gln Val Leu Leu Glu Ile Lys
 580 585 590

30
 <210> 5
 <211> 2128
 <212> DNA
 35 <213> *Corynebacterium thermoaminogenes*

<220>
 <221> CDS
 40 <222> (339).. (1967)

<400> 5
 45 gcgltcattc cgaccacatt cgccccggga lccgggcicc accacciccc ggaccatgc 60
 cccataccig cggaaccac gggaaacac ggaaaaaccg atcicattca gaccggcggg 120
 atccaccigl ggaacagica gcggcgcggc catggagggc agcgacaggi gacgtccgag 180
 cacccggltc cccaccgigg acacggcatt gatccgacac ggiggggata gtlitcagcl 240
 gaaaaactat cgcigtgcag ggaggatccg gaatlgigacc tatttcattg agaaatgatt 300
 50 gttgacgata cccccgggta cggctaccat tccaaaac atg acc att tcc tca cct 356
 Met Thr Ile Ser Ser Pro
 1 5
 55 ttg att gac gic gct aac ctg cca gac atc aac acc acc gcc ggc aag 404
 Leu Ile Asp Val Ala Asn Leu Pro Asp Ile Asn Thr Thr Ala Gly Lys

| | | | | |
|----|---|------|----|--|
| | 10 | 15 | 20 | |
| | atc gcc gac ctg aag gcc cgc cgg ggc gaa gcc cac ttc ccc atg ggt | 452 | | |
| 5 | Ile Ala Asp Leu Lys Ala Arg Arg Ala Glu Ala His Phe Pro Met Gly | | | |
| | 25 30 35 | | | |
| | gaa aag gcc gta gag aag gtc cac ggc gcc aac cgc ctc acc ggc cgc | 500 | | |
| | Glu Lys Ala Val Glu Lys Val His Ala Ala Asn Arg Leu Thr Ala Arg | | | |
| 10 | 40 45 50 | | | |
| | gaa cga ctt gac tac ctg ctc gat gaa ggc tcc ttc atc gaa acc gat | 548 | | |
| | Glu Arg Leu Asp Tyr Leu Leu Asp Glu Gly Ser Phe Ile Glu Thr Asp | | | |
| | 55 60 65 70 | | | |
| 15 | cag ctc gca cgc cac cgc acc acc ggc ttc ggc ctg ggc aac aag cga | 596 | | |
| | Gln Leu Ala Arg His Arg Thr Thr Ala Phe Gly Leu Gly Asn Lys Arg | | | |
| | 75 80 85 | | | |
| | ccg gcc acc gac ggc atc gtc acc ggc tgg ggc acc atc gac ggc cgc | 644 | | |
| 20 | Pro Ala Thr Asp Gly Ile Val Thr Gly Trp Gly Thr Ile Asp Gly Arg | | | |
| | 90 95 100 | | | |
| | gag gtc tgc atc ttc tcc cag gac ggc acc gtc ttc ggt ggc gca ctc | 692 | | |
| | Glu Val Cys Ile Phe Ser Gln Asp Gly Thr Val Phe Gly Gly Ala Leu | | | |
| 25 | 105 110 115 | | | |
| | ggt gag gtc tac ggc gag aag atg atc aag atc atg gag ctg gcc atc | 740 | | |
| | Gly Glu Val Tyr Gly Glu Lys Met Ile Lys Ile Met Glu Leu Ala Ile | | | |
| | 120 125 130 | | | |
| 30 | gac acc ggc cgc cca ctc atc ggc ctg tac gag ggt gca ggt gcc cgc | 788 | | |
| | Asp Thr Gly Arg Pro Leu Ile Gly Leu Tyr Glu Gly Ala Gly Ala Arg | | | |
| | 135 140 145 150 | | | |
| | atc cag gac ggt ggc gtc tcc ctc gac ttc atc tcc cag acc ttc tat | 836 | | |
| 35 | Ile Gln Asp Gly Ala Val Ser Leu Asp Phe Ile Ser Gln Thr Phe Tyr | | | |
| | 155 160 165 | | | |
| | cag aac atc cag gcc tcc ggc gtg atc ccg cag atc tcc gtg atc atg | 884 | | |
| | Gln Asn Ile Gln Ala Ser Gly Val Ile Pro Gln Ile Ser Val Ile Met | | | |
| 40 | 170 175 180 | | | |
| | ggt gcc tgc gcc ggt ggc aac gcc tac ggc ccg gcc ctg acc gac ttc | 932 | | |
| | Gly Ala Cys Ala Gly Gly Asn Ala Tyr Gly Pro Ala Leu Thr Asp Phe | | | |
| | 185 190 195 | | | |
| 45 | gtg gtc atg gtg gac aag acc tgc aag atg ttc gtc acc ggc ccc gat | 980 | | |
| | Val Val Met Val Asp Lys Thr Ser Lys Met Phe Val Thr Gly Pro Asp | | | |
| | 200 205 210 | | | |
| | gtg atc aag acc gtc acc ggc gag gag atc acc cag gag gag ctc ggc | 1028 | | |
| 50 | Val Ile Lys Thr Val Thr Gly Glu Glu Ile Thr Gln Glu Glu Leu Gly | | | |
| | 215 220 225 230 | | | |
| | gga gca acc acc cac atg gtc acc gcc ggc aac tcc cac tac acc gtc | 1076 | | |
| | Gly Ala Thr Thr His Met Val Thr Ala Gly Asn Ser His Tyr Thr Val | | | |
| 55 | 235 240 245 | | | |

gcc acc gat gag gag gcc ctc gac tgg gtc cag gac ctc atc tcc ttc 1124
 Ala Thr Asp Glu Glu Ala Leu Asp Trp Val Gln Asp Leu Ile Ser Phe
 250 255 260
 5 ctc ccc tcc aac aat cgc tcc tac gcc ccg gtg gag gag ttc gac gag 1172
 Leu Pro Ser Asn Asn Arg Ser Tyr Ala Pro Val Glu Glu Phe Asp Glu
 265 270 275
 10 gag gac ggt ggc atc gcc gag aac atc acc gcc gat gac ctg aag ctg 1220
 Glu Asp Gly Gly Ile Ala Glu Asn Ile Thr Ala Asp Asp Leu Lys Leu
 280 285 290
 gat gag atc atc ccg gat tcc gcc acc gtg ccc tat gat gtc cgc gac 1268
 15 Asp Glu Ile Ile Pro Asp Ser Ala Thr Val Pro Tyr Asp Val Arg Asp
 295 300 305 310
 gtc atc cag tgc ctg acc gac gac ggt gag tac ctg gag atc cag gcc 1316
 Val Ile Gln Cys Leu Thr Asp Asp Gly Glu Tyr Leu Glu Ile Gln Ala
 315 320 325
 20 gac cga gcc gag aat gtc gtc atc gcc ttc ggc cgc atc gag ggc cag 1364
 Asp Arg Ala Glu Asn Val Val Ile Ala Phe Gly Arg Ile Glu Gly Gln
 330 335 340
 25 tcc gtc ggt ttc gtc gcc aac cag ccg acc cag ttc gcc ggc tgc ctg 1412
 Ser Val Gly Phe Val Ala Asn Gln Pro Thr Gln Phe Ala Gly Cys Leu
 345 350 355
 gac atc gac tcc tcc gag aag gca gcc cgc ttc gtc cgc acc tgc gat 1460
 30 Asp Ile Asp Ser Ser Glu Lys Ala Ala Arg Phe Val Arg Thr Cys Asp
 360 365 370
 gcc ttc aac atc ccg atc gtc atg ctt gtc gac gtc ccc ggc ttc ctc 1508
 Ala Phe Asn Ile Pro Ile Val Met Leu Val Asp Val Pro Gly Phe Leu
 375 380 385 390
 35 ccc ggt gcc ggc cag gag tac ggc ggc atc ctg cgt cgt ggc gcc aaa 1556
 Pro Gly Ala Gly Gln Glu Tyr Gly Gly Ile Leu Arg Arg Gly Ala Lys
 395 400 405
 40 ctg ctc tac gcc tac ggt gag gcc acc gtc ccg aag atc acc gtg acc 1604
 Leu Leu Tyr Ala Tyr Gly Glu Ala Thr Val Pro Lys Ile Thr Val Thr
 410 415 420
 atg cgc aag gcc tac ggc ggt gcg tac tgt gtc atg gga tcc aag ggt 1652
 45 Met Arg Lys Ala Tyr Gly Gly Ala Tyr Cys Val Met Gly Ser Lys Gly
 425 430 435
 ctg ggc gca gac atc aac ctg gcc tgg ccg acc gcg cag atc gcc gtc 1700
 50 Leu Gly Ala Asp Ile Asn Leu Ala Trp Pro Thr Ala Gln Ile Ala Val
 440 445 450
 atg ggt gcc gcc ggc gcg gtc cag ttc atc tac cgc aag gag ctc atg 1748
 Met Gly Ala Ala Gly Ala Val Gln Phe Ile Tyr Arg Lys Glu Leu Met
 455 460 465 470
 55 gcc gcl gat gcc aag ggc ctg gac acc gtc gcc ctg gcc cag tcc ttc 1796

Ala Ala Asp Ala Lys Gly Leu Asp Thr Val Ala Leu Ala Gln Ser Phe

475

480

485

gag cgt gag tac gag gac cac atg ctc aac ccg tac ctg gcg gcc gag 1844

Glu Arg Glu Tyr Glu Asp His Met Leu Asn Pro Tyr Leu Ala Ala Glu

490

495

500

cgt ggc ctc atc gac gcg gtg atc ctg ccg tcc gag acc cgt ggc cag 1892

Arg Gly Leu Ile Asp Ala Val Ile Leu Pro Ser Glu Thr Arg Gly Gln

505

510

515

atc gca cgc aac ctg cgt ctg ctc aag cac aag aat gtc tcc cgc cct 1940

Ile Ala Arg Asn Leu Arg Leu Leu Lys His Lys Asn Val Ser Arg Pro

520

525

530

gcc cgc aag cac ggc aac atg cca ctg taagcaccg ggaccacccc 1987

Ala Arg Lys His Gly Asn Met Pro Leu

535 540

ctacgcccgc acccaggcc ctctgctggc aggtgcgggc gctgtgcgtt ttccgcgcct 2047

gccgacgcc ggccccctgc cctgtgatgc gatctgcgga tgtgatctgc gccgcgcga 2107

actccccigg ttgaacctg c 2128

<210> 6

<211> 543

<212> PRT

<213> Corynebacterium thermoaminogenes

<400> 6

Met Thr Ile Ser Ser Pro Leu Ile Asp Val Ala Asn Leu Pro Asp Ile

1

5

10

15

Asn Thr Thr Ala Gly Lys Ile Ala Asp Leu Lys Ala Arg Arg Ala Glu

20

25

30

Ala His Phe Pro Met Gly Glu Lys Ala Val Glu Lys Val His Ala Ala

35

40

45

Asn Arg Leu Thr Ala Arg Glu Arg Leu Asp Tyr Leu Leu Asp Glu Gly

50

55

60

Ser Phe Ile Glu Thr Asp Gln Leu Ala Arg His Arg Thr Thr Ala Phe

65

70

75

80

Gly Leu Gly Asn Lys Arg Pro Ala Thr Asp Gly Ile Val Thr Gly Trp

85

90

95

Gly Thr Ile Asp Gly Arg Glu Val Cys Ile Phe Ser Gln Asp Gly Thr

100

105

110

Val Phe Gly Gly Ala Leu Gly Glu Val Tyr Gly Glu Lys Met Ile Lys

115

120

125

Ile Met Glu Leu Ala Ile Asp Thr Gly Arg Pro Leu Ile Gly Leu Tyr

130

135

140

Glu Gly Ala Gly Ala Arg Ile Gln Asp Gly Ala Val Ser Leu Asp Phe

145 150 155 160
 Ile Ser Gln Thr Phe Tyr Gln Asn Ile Gln Ala Ser Gly Val Ile Pro
 5 165 170 175
 Gln Ile Ser Val Ile Met Gly Ala Cys Ala Gly Gly Asn Ala Tyr Gly
 180 185 190
 Pro Ala Leu Thr Asp Phe Val Val Met Val Asp Lys Thr Ser Lys Met
 10 195 200 205
 Phe Val Thr Gly Pro Asp Val Ile Lys Thr Val Thr Gly Glu Glu Ile
 210 215 220
 Thr Gln Glu Glu Leu Gly Gly Ala Thr Thr His Met Val Thr Ala Gly
 15 225 230 235 240
 Asn Ser His Tyr Thr Val Ala Thr Asp Glu Glu Ala Leu Asp Trp Val
 245 250 255
 Gln Asp Leu Ile Ser Phe Leu Pro Ser Asn Asn Arg Ser Tyr Ala Pro
 20 260 265 270
 Val Glu Glu Phe Asp Glu Glu Asp Gly Gly Ile Ala Glu Asn Ile Thr
 275 280 285
 Ala Asp Asp Leu Lys Leu Asp Glu Ile Ile Pro Asp Ser Ala Thr Val
 25 290 295 300
 Pro Tyr Asp Val Arg Asp Val Ile Gln Cys Leu Thr Asp Asp Gly Glu
 305 310 315 320
 Tyr Leu Glu Ile Gln Ala Asp Arg Ala Glu Asn Val Val Ile Ala Phe
 30 325 330 335
 Gly Arg Ile Glu Gly Gln Ser Val Gly Phe Val Ala Asn Gln Pro Thr
 340 345 350
 Gln Phe Ala Gly Cys Leu Asp Ile Asp Ser Ser Glu Lys Ala Ala Arg
 35 355 360 365
 Phe Val Arg Thr Cys Asp Ala Phe Asn Ile Pro Ile Val Met Leu Val
 370 375 380
 Asp Val Pro Gly Phe Leu Pro Gly Ala Gly Gln Glu Tyr Gly Gly Ile
 40 385 390 395 400
 Leu Arg Arg Gly Ala Lys Leu Leu Tyr Ala Tyr Gly Glu Ala Thr Val
 405 410 415
 Pro Lys Ile Thr Val Thr Met Arg Lys Ala Tyr Gly Gly Ala Tyr Cys
 45 420 425 430
 Val Met Gly Ser Lys Gly Leu Gly Ala Asp Ile Asn Leu Ala Trp Pro
 435 440 445
 Thr Ala Gln Ile Ala Val Met Gly Ala Ala Gly Ala Val Gln Phe Ile
 50 450 455 460
 Tyr Arg Lys Glu Leu Met Ala Ala Asp Ala Lys Gly Leu Asp Thr Val
 465 470 475 480
 Ala Leu Ala Gln Ser Phe Glu Arg Glu Tyr Glu Asp His Met Leu Asn
 55 485 490 495

Pro Tyr Leu Ala Ala Glu Arg Gly Leu Ile Asp Ala Val Ile Leu Pro

500

505

510

Ser Glu Thr Arg Gly Gln Ile Ala Arg Asn Leu Arg Leu Leu Lys His

515

520

525

Lys Asn Val Ser Arg Pro Ala Arg Lys His Gly Asn Met Pro Leu

530

535

540

<210> 7

<211> 2076

<212> DNA

<213> *Corynebacterium thermoaminogenes*

<220>

<221> CDS

<222> (412)..(2022)

<400> 7

acgcccggcc ccccgcccg tgaigcgaic tgcggaigtg atcigcgccc gcgccaactc 60

ccciggttga acccigccac ataccctgag tgcaccctgg gtggggicac ttccacctc 120

acggggggga ggagglicaca taggccatac gctgcacitl lgaigaagtg tggcagatc 180

gaccgggcaa atcigggaaa taaggggcci ggigaactag catlccccit agcgaagggt 240

gagcaticcg gaccccgga tgcaccaacc ggicgtaaat lcalgtgccg ccacagtc 300

ctcaccaggg gatcggaacc agcccagcct galiccgcg tgcaggacct caccgigaac 360

aagtccccg c attactcaca gaactcacac caggatitag actaagaac c atg act 417

Met Thr

1

gca gca acg aca gca cct gat ctg acc acc acc gcc ggc aaa ctg cgc 465

Ala Ala Thr Thr Ala Pro Asp Leu Thr Thr Thr Ala Gly Lys Leu Ala

5

10

15

gat ctg cgc gcc cgc ctg tcc gag acc cag gcc ccc atg ggt cag gcc 513

Asp Leu Arg Ala Arg Leu Ser Glu Thr Gln Ala Pro Met Gly Gln Ala

20

25

30

icc glg gag aag glg cac gag gca ggg aag aag acc gca cgc gag cgc 561

Ser Val Glu Lys Val His Glu Ala Gly Lys Lys Thr Ala Arg Glu Arg

35

40

45

50

alc gag tac ctg ctg gat gag ggc tcc ttc gtt gag gtc gat gcc ctg 609

Ile Glu Tyr Leu Leu Asp Glu Gly Ser Phe Val Glu Val Asp Ala Leu

55

60

65

gcc cgc cac cgt tcc aag aac ttc ggc ctg gac tcc aag cgc ccg gtc 657

Ala Arg His Arg Ser Lys Asn Phe Gly Leu Asp Ser Lys Arg Pro Val

70

75

80

acc gac ggt glg gtc acc ggt tac ggc acc alc gac gga cgc aag gtc 705

Thr Asp Gly Val Val Thr Gly Tyr Gly Thr Ile Asp Gly Arg Lys Val

| | | | | |
|----|---|-----|-----|------|
| | 85 | 90 | 95 | |
| | tgc gtc ttc tcc cag gac ggc gct atc ttc ggc ggt gcc ctc ggt gag | | | 753 |
| 5 | Cys Val Phe Ser Gln Asp Gly Ala Ile Phe Gly Gly Ala Leu Gly Glu | | | |
| | 100 | 105 | 110 | |
| | gtc tac ggc gag aag atc gtc aag atc atg gac ctg gcc atc aag acc | | | 801 |
| | Val Tyr Gly Glu Lys Ile Val Lys Ile Met Asp Leu Ala Ile Lys Thr | | | |
| 10 | 115 | 120 | 125 | 130 |
| | ggt gtc ccc ctc atc ggc atc aac gag ggc gcc ggc gcc cgc atc cag | | | 849 |
| | Gly Val Pro Leu Ile Gly Ile Asn Glu Gly Ala Gly Ala Arg Ile Gln | | | |
| | 135 | 140 | 145 | |
| 15 | gaa ggc gtt gtc tcc ctg ggc ctg tac tcc cag atc ttc tac cgc aac | | | 897 |
| | Glu Gly Val Val Ser Leu Gly Leu Tyr Ser Gln Ile Phe Tyr Arg Asn | | | |
| | 150 | 155 | 160 | |
| | acc cag gca tcc ggt gtc atc cca cag atc tcc ctc atc atg ggt gcc | | | 945 |
| 20 | Thr Gln Ala Ser Gly Val Ile Pro Gln Ile Ser Leu Ile Met Gly Ala | | | |
| | 165 | 170 | 175 | |
| | tgc gcc ggt ggc cat gtg tac tcc ccc gcc ctg acc gac ttc atc atc | | | 993 |
| | Cys Ala Gly Gly His Val Tyr Ser Pro Ala Leu Thr Asp Phe Ile Ile | | | |
| 25 | 180 | 185 | 190 | |
| | atg gtg gac aag acc tcc aag atg ttc atc acc ggc ccc gac gtg atc | | | 1041 |
| | Met Val Asp Lys Thr Ser Lys Met Phe Ile Thr Gly Pro Asp Val Ile | | | |
| | 195 | 200 | 205 | 210 |
| 30 | aag acc gtc acc ggc gag gag gtc acc cag gag gaa ctg ggt ggt gcc | | | 1089 |
| | Lys Thr Val Thr Gly Glu Glu Val Thr Gln Glu Glu Leu Gly Gly Ala | | | |
| | 215 | 220 | 225 | |
| | tac acc cac atg gcc cag tcc ggc acc tgc cac tac acc gca gcc gat | | | 1137 |
| 35 | Tyr Thr His Met Ala Gln Ser Gly Thr Ser His Tyr Thr Ala Ala Asp | | | |
| | 230 | 235 | 240 | |
| | gac tcc gat gcc ctc gac tgg gtc cgt gag ctg gtc agc tac ctg ccg | | | 1185 |
| | Asp Ser Asp Ala Leu Asp Trp Val Arg Glu Leu Val Ser Tyr Leu Pro | | | |
| 40 | 245 | 250 | 255 | |
| | tcc aac aac cgt gcg gag acc cca cgc cag gac gcc gac atc atg gtg | | | 1233 |
| | Ser Asn Asn Arg Ala Glu Thr Pro Arg Gln Asp Ala Asp Ile Met Val | | | |
| | 260 | 265 | 270 | |
| 45 | ggc tcc atc aag gag aac atc acc gag acc gac ctc gaa ctc gac acc | | | 1281 |
| | Gly Ser Ile Lys Glu Asn Ile Thr Glu Thr Asp Leu Glu Leu Asp Thr | | | |
| | 275 | 280 | 285 | 290 |
| | ctg atc ccg gat tcc ccg aac cag ccg tac gac atg aag gac gtc atc | | | 1329 |
| 50 | Leu Ile Pro Asp Ser Pro Asn Gln Pro Tyr Asp Met Lys Asp Val Ile | | | |
| | 295 | 300 | 305 | |
| | acc cgc atc gtc gat gat gcc gag ttc ttc gag atc cag gag ggt tac | | | 1377 |
| 55 | Thr Arg Ile Val Asp Asp Ala Glu Phe Phe Glu Ile Gln Glu Gly Tyr | | | |
| | 310 | 315 | 320 | |

| | | |
|----|---|------|
| | gcc gag aac atc atc tgc ggt ttc gcc cgc gtc gag ggt cgt gcc gtg | 1425 |
| | Ala Glu Asn Ile Ile Cys Gly Phe Ala Arg Val Glu Gly Arg Ala Val | |
| | 325 330 335 | |
| 5 | ggt atc gtc gcc aac cag ccg atg cag ttc gcc ggc tgc ctg gac atc | 1473 |
| | Gly Ile Val Ala Asn Gln Pro Met Gln Phe Ala Gly Cys Leu Asp Ile | |
| | 340 345 350 | |
| 10 | aag gca tcc gag aag gcc gcc cgc ttc atc cgc acc tgt gac gcc ttc | 1521 |
| | Lys Ala Ser Glu Lys Ala Ala Arg Phe Ile Arg Thr Cys Asp Ala Phe | |
| | 355 360 365 370 | |
| 15 | aac atc ccg atc atc gag ctt gtc gac gtc cca ggc ttc ctc ccg ggc | 1569 |
| | Asn Ile Pro Ile Ile Glu Leu Val Asp Val Pro Gly Phe Leu Pro Gly | |
| | 375 380 385 | |
| | acc aac cag gag ttc gac ggc atc atc cgt cgc ggc gcg aag ctg ctc | 1617 |
| | Thr Asn Gln Glu Phe Asp Gly Ile Ile Arg Arg Gly Ala Lys Leu Leu | |
| | 390 395 400 | |
| 20 | tac gcc tac gcc gag gcc acc gtc ggc aag atc acc gtg atc acc cgc | 1665 |
| | Tyr Ala Tyr Ala Glu Ala Thr Val Gly Lys Ile Thr Val Ile Thr Arg | |
| | 405 410 415 | |
| 25 | aag tcc tac ggc ggt gcc tac tgc gtg atg ggc tcc aag gac atg ggt | 1713 |
| | Lys Ser Tyr Gly Gly Ala Tyr Cys Val Met Gly Ser Lys Asp Met Gly | |
| | 420 425 430 | |
| 30 | gcg gac ctc gtc ttc gca tgg ccc acc gcg cag atc gcc gtc atg ggt | 1761 |
| | Ala Asp Leu Val Phe Ala Trp Pro Thr Ala Gln Ile Ala Val Met Gly | |
| | 435 440 445 450 | |
| | gcc tcc ggt gcc gtc ggc ttc atc tac cgc aag gag ctc aag cag gct | 1809 |
| | Ala Ser Gly Ala Val Gly Phe Ile Tyr Arg Lys Glu Leu Lys Gln Ala | |
| | 455 460 465 | |
| 35 | gca gcg gcc ggc gag gat gtc acc gcg ctg atg aag aag tac gag cag | 1857 |
| | Ala Ala Ala Gly Glu Asp Val Thr Ala Leu Met Lys Lys Tyr Glu Gln | |
| | 470 475 480 | |
| 40 | gag tac gag gag acc ctg gtc aac ccg tac atg gct gca gag cgt ggc | 1905 |
| | Glu Tyr Glu Glu Thr Leu Val Asn Pro Tyr Met Ala Ala Glu Arg Gly | |
| | 485 490 495 | |
| 45 | tac gtc gac gcc gtc atc cca cca tcc gag acc cgt ggt cag atc atc | 1953 |
| | Tyr Val Asp Ala Val Ile Pro Pro Ser Glu Thr Arg Gly Gln Ile Ile | |
| | 500 505 510 | |
| | gag ggt ctg cgt ctg ctc gac cgc aag gtg gtc aac gtc ccg gcc aag | 2001 |
| | Glu Gly Leu Arg Leu Leu Asp Arg Lys Val Val Asn Val Pro Ala Lys | |
| | 515 520 525 530 | |
| 50 | aag cac ggt aac atc ccg ctg taaaccgtct tcccctccgg caccacgccg | 2052 |
| | Lys His Gly Asn Ile Pro Leu | |
| | 535 | |
| 55 | gagaaggcct tgcgccgac tgc | 2076 |

<210> 8

<211> 537

<212> PRT

<213> *Corynebacterium thermoaminogenes*

<400> 8

Met Thr Ala Ala Thr Thr Ala Pro Asp Leu Thr Thr Thr Ala Gly Lys
 1 5 10 15
 Leu Ala Asp Leu Arg Ala Arg Leu Ser Glu Thr Gln Ala Pro Met Gly
 20 25 30
 Gln Ala Ser Val Glu Lys Val His Glu Ala Gly Lys Lys Thr Ala Arg
 35 40 45
 Glu Arg Ile Glu Tyr Leu Leu Asp Glu Gly Ser Phe Val Glu Val Asp
 50 55 60
 Ala Leu Ala Arg His Arg Ser Lys Asn Phe Gly Leu Asp Ser Lys Arg
 65 70 75 80
 Pro Val Thr Asp Gly Val Val Thr Gly Tyr Gly Thr Ile Asp Gly Arg
 85 90 95
 Lys Val Cys Val Phe Ser Gln Asp Gly Ala Ile Phe Gly Gly Ala Leu
 100 105 110
 Gly Glu Val Tyr Gly Glu Lys Ile Val Lys Ile Met Asp Leu Ala Ile
 115 120 125
 Lys Thr Gly Val Pro Leu Ile Gly Ile Asn Glu Gly Ala Gly Ala Arg
 130 135 140
 Ile Gln Glu Gly Val Val Ser Leu Gly Leu Tyr Ser Gln Ile Phe Tyr
 145 150 155 160
 Arg Asn Thr Gln Ala Ser Gly Val Ile Pro Gln Ile Ser Leu Ile Met
 165 170 175
 Gly Ala Cys Ala Gly Gly His Val Tyr Ser Pro Ala Leu Thr Asp Phe
 180 185 190
 Ile Ile Met Val Asp Lys Thr Ser Lys Met Phe Ile Thr Gly Pro Asp
 195 200 205
 Val Ile Lys Thr Val Thr Gly Glu Glu Val Thr Gln Glu Glu Leu Gly
 210 215 220
 Gly Ala Tyr Thr His Met Ala Gln Ser Gly Thr Ser His Tyr Thr Ala
 225 230 235 240
 Ala Asp Asp Ser Asp Ala Leu Asp Trp Val Arg Glu Leu Val Ser Tyr
 245 250 255
 Leu Pro Ser Asn Asn Arg Ala Glu Thr Pro Arg Gln Asp Ala Asp Ile
 260 265 270
 Met Val Gly Ser Ile Lys Glu Asn Ile Thr Glu Thr Asp Leu Glu Leu
 275 280 285

| | | | | | | | | | | | | | | | | |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| | Asp | Thr | Leu | Ile | Pro | Asp | Ser | Pro | Asn | Gln | Pro | Tyr | Asp | Met | Lys | Asp |
| | 290 | | | | | | 295 | | | | | 300 | | | | |
| 5 | Val | Ile | Thr | Arg | Ile | Val | Asp | Asp | Ala | Glu | Phe | Phe | Glu | Ile | Gln | Glu |
| | 305 | | | | | 310 | | | | | 315 | | | | | 320 |
| | Gly | Tyr | Ala | Glu | Asn | Ile | Ile | Cys | Gly | Phe | Ala | Arg | Val | Glu | Gly | Arg |
| | | | | | 325 | | | | | 330 | | | | | 335 | |
| 10 | Ala | Val | Gly | Ile | Val | Ala | Asn | Gln | Pro | Met | Gln | Phe | Ala | Gly | Cys | Leu |
| | | | | 340 | | | | | 345 | | | | | 350 | | |
| | Asp | Ile | Lys | Ala | Ser | Glu | Lys | Ala | Ala | Arg | Phe | Ile | Arg | Thr | Cys | Asp |
| | | | 355 | | | | | 360 | | | | | 365 | | | |
| 15 | Ala | Phe | Asn | Ile | Pro | Ile | Ile | Glu | Leu | Val | Asp | Val | Pro | Gly | Phe | Leu |
| | 370 | | | | | | 375 | | | | | 380 | | | | |
| | Pro | Gly | Thr | Asn | Gln | Glu | Phe | Asp | Gly | Ile | Ile | Arg | Arg | Gly | Ala | Lys |
| | 385 | | | | | 390 | | | | | 395 | | | | | 400 |
| 20 | Leu | Leu | Tyr | Ala | Tyr | Ala | Glu | Ala | Thr | Val | Gly | Lys | Ile | Thr | Val | Ile |
| | | | | 405 | | | | | | 410 | | | | | 415 | |
| | Thr | Arg | Lys | Ser | Tyr | Gly | Gly | Ala | Tyr | Cys | Val | Met | Gly | Ser | Lys | Asp |
| | | | | 420 | | | | 425 | | | | | | 430 | | |
| 25 | Met | Gly | Ala | Asp | Leu | Val | Phe | Ala | Trp | Pro | Thr | Ala | Gln | Ile | Ala | Val |
| | | 435 | | | | | 440 | | | | | | 445 | | | |
| | Met | Gly | Ala | Ser | Gly | Ala | Val | Gly | Phe | Ile | Tyr | Arg | Lys | Glu | Leu | Lys |
| | | 450 | | | | 455 | | | | | | 460 | | | | |
| 30 | Gln | Ala | Ala | Ala | Ala | Gly | Glu | Asp | Val | Thr | Ala | Leu | Met | Lys | Lys | Tyr |
| | 465 | | | | | 470 | | | | | 475 | | | | | 480 |
| | Glu | Gln | Glu | Tyr | Glu | Glu | Thr | Leu | Val | Asn | Pro | Tyr | Met | Ala | Ala | Glu |
| | | | | 485 | | | | | | 490 | | | | | 495 | |
| 35 | Arg | Gly | Tyr | Val | Asp | Ala | Val | Ile | Pro | Pro | Ser | Glu | Thr | Arg | Gly | Gln |
| | | | | 500 | | | | | 505 | | | | | 510 | | |
| | Ile | Ile | Glu | Gly | Leu | Arg | Leu | Leu | Asp | Arg | Lys | Val | Val | Asn | Val | Pro |
| | | | 515 | | | | | 520 | | | | | 525 | | | |
| 40 | Ala | Lys | Lys | His | Gly | Asn | Ile | Pro | Leu | | | | | | | |
| | | 530 | | | | | 535 | | | | | | | | | |

<210> 9

<211> 1643

<212> DNA

<213> Corynebacterium thermoaminogenes

<220>

<221> CDS

<222> (326).. (1363)

<400> 9

agcgcgccgg cagccaccag igggalcgig cccagcggac ggatgccgga ttcacggcgg 60
 tcagccaccc gccgatgaga cctgcagcga caacgggtgc ggtagcgacc tggcagcgt 120
 5 cttigagitt calatccalg tcagacagtc laaccactct ctcgacgcg tccgaacatg 180
 cigggggggc ggacaccatg tccgttcggg cgtlccccg acgggggaaa atcgaggca 240
 gatgtgiccg atgtgggata aaccaccgg ttcgggcgig tcttcgggat caatggcaca 300
 gcattaaccg tgiggggggg ttaat alg gga gcc alg cga att gcc act ctc 352
 10 Met Gly Ala Met Arg Ile Ala Thr Leu
 1 5
 acg tca ggc ggc gac igc ccc gga ctc aat gct gtc atc agg gga atc 400
 Thr Ser Gly Gly Asp Cys Pro Gly Leu Asn Ala Val Ile Arg Gly Ile
 15 10 15 20 25
 gtc cgt acc gca agt aat gaa ttc ggt tcc acc gtc gtg ggt tat cag 448
 Val Arg Thr Ala Ser Asn Glu Phe Gly Ser Thr Val Val Gly Tyr Gln
 30 35 40
 20 gac ggc igg gag ggc ctg ctg gcg gac cga cgt gtt cag ctc tat gac 496
 Asp Gly Trp Glu Gly Leu Leu Ala Asp Arg Arg Val Gln Leu Tyr Asp
 45 50 55
 gat gag gac atc gac cgc atc ctg ctc cgc ggt gga aca atc ctg ggc 544
 25 Asp Glu Asp Ile Asp Arg Ile Leu Leu Arg Gly Gly Thr Ile Leu Gly
 60 65 70
 acc ggt cgt ctc cac ccc gac aag ttc aga gcc gga atc gac cag gtc 592
 Thr Gly Arg Leu His Pro Asp Lys Phe Arg Ala Gly Ile Asp Gln Val
 30 75 80 85
 aag gcg aat ctc gcc gat gcg gga att gac gca ctc atc ccg atc ggt 640
 Lys Ala Asn Leu Ala Asp Ala Gly Ile Asp Ala Leu Ile Pro Ile Gly
 90 95 100 105
 35 ggc gag ggc acc ctc aag gga gcg aag tgg ctc gcc gac aac ggc atc 688
 Gly Glu Gly Thr Leu Lys Gly Ala Lys Trp Leu Ala Asp Asn Gly Ile
 110 115 120
 ccc gtg gtc ggt gtc ccg aaa acc atc gac aat gat gtc aac ggc acg 736
 40 Pro Val Val Gly Val Pro Lys Thr Ile Asp Asn Asp Val Asn Gly Thr
 125 130 135
 gat ttc acc ttc ggt ttc gat tcc gcg gtc tct gtg gcc acc gac gcc 784
 Asp Phe Thr Phe Gly Phe Asp Ser Ala Val Ser Val Ala Thr Asp Ala
 45 140 145 150
 atc gac cgg ctg cac acc acg gcg gaa tcc cac aac cgt gtg atg atc 832
 Ile Asp Arg Leu His Thr Thr Ala Glu Ser His Asn Arg Val Met Ile
 155 160 165
 50 gtc gag gtc atg ggc cgc cac gtc ggt tgg atc gca ctg cat gcc ggc 880
 Val Glu Val Met Gly Arg His Val Gly Trp Ile Ala Leu His Ala Gly
 170 175 180 185
 atg gcc ggt gga gcc cac tac acc gtc atc ccc gag gtg ccc ttc gac 928
 55 Met Ala Gly Gly Ala His Tyr Thr Val Ile Pro Glu Val Pro Phe Asp

190 195 200
 atc tgc gag atc tgc aag cgt atg gaa cgt cgc ttc cag atg ggg gag 976
 Ile Ser Glu Ile Cys Lys Arg Met Glu Arg Arg Phe Gln Met Gly Glu
 205 210 215
 aag tac ggc atc atc gtc gtc gcg gag ggt gcc ctg ccc aag gag gga 1024
 Lys Tyr Gly Ile Ile Val Val Ala Glu Gly Ala Leu Pro Lys Glu Gly
 220 225 230
 acc atg gag ctg cgt gag ggg gag gtg gat cag ttc ggt cac aag acc 1072
 Thr Met Glu Leu Arg Glu Gly Glu Val Asp Gln Phe Gly His Lys Thr
 235 240 245
 ttc acc ggc atc ggc cag cag atc gcc gac gag gtg cac agg cgt ctg 1120
 Phe Thr Gly Ile Gly Gln Gln Ile Ala Asp Glu Val His Arg Arg Leu
 250 255 260 265
 ggt cat gat gtc cgc acc acg gtc ctg ggc cat atc cag cgt ggt ggc 1168
 Gly His Asp Val Arg Thr Thr Val Leu Gly His Ile Gln Arg Gly Gly
 270 275 280
 acc ccc acc gcc ttc gac cgt gtc ctg gcc acc cgg tac ggt gtc cgc 1216
 Thr Pro Thr Ala Phe Asp Arg Val Leu Ala Thr Arg Tyr Gly Val Arg
 285 290 295
 gcc gcg cgt gcc tgc cac gag ggt cag ttc aac acc gtg gtc gcg ctc 1264
 Ala Ala Arg Ala Cys His Glu Gly Gln Phe Asn Thr Val Val Ala Leu
 300 305 310
 aag ggg gag cgc atc cgg atg atc tcc ttc gat gag gcc gtg ggc acc 1312
 Lys Gly Glu Arg Ile Arg Met Ile Ser Phe Asp Glu Ala Val Gly Thr
 315 320 325
 ctg aag aag gtg ccg atg gaa cgc tgg gtg acc gcc cag gct atg ttc 1360
 Leu Lys Lys Val Pro Met Glu Arg Trp Val Thr Ala Gln Ala Met Phe
 330 335 340 345
 ggt tagtcaggcc gcatcccggt ttcgcgcgcc gcggggccgg gtittttcat 1413
 Gly
 gccccggaac acatcggtat gaaatcgiga taigcattac ttgacgggga agtgggggat 1473
 ccgtcaccic gcgttgicca actacagccc gcagcgccig cggaattct tgcagcaatc 1533
 cgccgattec ccggcccgic ccgtcgccgt ccaaccgcag tacaatctgc tggcccgccg 1593
 ggattatgag accggtatcc gcccggtcgt ggacgagtic ggtcccgccg 1643
 45
 <210> 10
 <211> 346
 <212> PRT
 50 <213> Corynebacterium thermoaminogenes
 <400> 10
 Met Gly Ala Met Arg Ile Ala Thr Leu Thr Ser Gly Gly Asp Cys Pro
 55 1 5 10 15

Gly Leu Asn Ala Val Ile Arg Gly Ile Val Arg Thr Ala Ser Asn Glu
 20 25 30
 5 Phe Gly Ser Thr Val Val Gly Tyr Gln Asp Gly Trp Glu Gly Leu Leu
 35 40 45
 Ala Asp Arg Arg Val Gln Leu Tyr Asp Asp Glu Asp Ile Asp Arg Ile
 50 55 60
 10 Leu Leu Arg Gly Gly Thr Ile Leu Gly Thr Gly Arg Leu His Pro Asp
 65 70 75 80
 Lys Phe Arg Ala Gly Ile Asp Gln Val Lys Ala Asn Leu Ala Asp Ala
 85 90 95
 15 Gly Ile Asp Ala Leu Ile Pro Ile Gly Gly Glu Gly Thr Leu Lys Gly
 100 105 110
 Ala Lys Trp Leu Ala Asp Asn Gly Ile Pro Val Val Gly Val Pro Lys
 115 120 125
 20 Thr Ile Asp Asn Asp Val Asn Gly Thr Asp Phe Thr Phe Gly Phe Asp
 130 135 140
 Ser Ala Val Ser Val Ala Thr Asp Ala Ile Asp Arg Leu His Thr Thr
 145 150 155 160
 25 Ala Glu Ser His Asn Arg Val Met Ile Val Glu Val Met Gly Arg His
 165 170 175
 Val Gly Trp Ile Ala Leu His Ala Gly Met Ala Gly Gly Ala His Tyr
 180 185 190
 30 Thr Val Ile Pro Glu Val Pro Phe Asp Ile Ser Glu Ile Cys Lys Arg
 195 200 205
 Met Glu Arg Arg Phe Gln Met Gly Glu Lys Tyr Gly Ile Ile Val Val
 210 215 220
 35 Ala Glu Gly Ala Leu Pro Lys Glu Gly Thr Met Glu Leu Arg Glu Gly
 225 230 235 240
 Glu Val Asp Gln Phe Gly His Lys Thr Phe Thr Gly Ile Gly Gln Gln
 245 250 255
 40 Ile Ala Asp Glu Val His Arg Arg Leu Gly His Asp Val Arg Thr Thr
 260 265 270
 Val Leu Gly His Ile Gln Arg Gly Gly Thr Pro Thr Ala Phe Asp Arg
 275 280 285
 45 Val Leu Ala Thr Arg Tyr Gly Val Arg Ala Ala Arg Ala Cys His Glu
 290 295 300
 Gly Gln Phe Asn Thr Val Val Ala Leu Lys Gly Glu Arg Ile Arg Met
 305 310 315 320
 50 Ile Ser Phe Asp Glu Ala Val Gly Thr Leu Lys Lys Val Pro Met Glu
 325 330 335
 Arg Trp Val Thr Ala Gln Ala Met Phe Gly
 340 345

<210> 11

<211> 498

<212> DNA

<213> *Corynebacterium thermoaminogenes*

<220>

<221> CDS

<222> (1)..(498)

<400> 11

```

15  lac tac cag cac gat cca ggt ttc ccc ttc gca cca aag cgc acc ggt 48
    Tyr Tyr Gln His Asp Pro Gly Phe Pro Phe Ala Pro Lys Arg Thr Gly
    1      5      10      15
20  tgg gct cac acc acc acg ccg ttg acc gga ccg cag cga ttg cag tgg 96
    Trp Ala His Thr Thr Thr Pro Leu Thr Gly Pro Gln Arg Leu Gln Trp
    20      25      30
25  acg cac ctg ccc gat gct ctt tac ccg gat gta tcc tat gac ctg gat 144
    Thr His Leu Pro Asp Ala Leu Tyr Pro Asp Val Ser Tyr Asp Leu Asp
    35      40      45
30  gga tgc tat tcc ggc gga gcc gta ttt tct gac ggc acg ctt aaa ctt 192
    Gly Cys Tyr Ser Gly Gly Ala Val Phe Ser Asp Gly Thr Leu Lys Leu
    50      55      60
35  ttc tac acc ggc aac cga aaa att gac ggc aag cgc cgc gcc acc caa 240
    Phe Tyr Thr Gly Asn Arg Lys Ile Asp Gly Lys Arg Arg Ala Thr Gln
    65      70      75      80
40  aac ctg gtc gaa gtc gag gac cca act ggg ctg atg ggc ggc att cat 288
    Asn Leu Val Glu Val Glu Asp Pro Thr Gly Leu Met Gly Gly Ile His
    85      90      95
45  cgc cgc tgc cct aaa aat ccg ctt atc gac gga ccc gcc agc ggt ttt 336
    Arg Arg Ser Pro Lys Asn Pro Leu Ile Asp Gly Pro Ala Ser Gly Phe
    100      105      110
50  acg ccc cac tac cgc gat ccc atg atc agc cct gat ggg gat ggt tgg 384
    Thr Pro His Tyr Arg Asp Pro Met Ile Ser Pro Asp Gly Asp Gly Trp
    115      120      125
55  aag atg gtt ctt ggg gct cag cgc gaa aac ctg acc ggt gca gcg gtt 432
    Lys Met Val Leu Gly Ala Gln Arg Glu Asn Leu Thr Gly Ala Ala Val
    130      135      140
60  cta tac cgc tgc gca gat ctt gaa aac tgg gaa ttc tcc ggt gaa atc 480
    Leu Tyr Arg Ser Ala Asp Leu Glu Asn Trp Glu Phe Ser Gly Glu Ile
    145      150      155      160
65  acc ttt gac ctg agc gac 498
    Thr Phe Asp Leu Ser Asp
    165

```

<210> 12
 <211> 166
 <212> PRT
 <213> Corynebacterium thermoaminogenes

<400> 12

Tyr Tyr Gln His Asp Pro Gly Phe Pro Phe Ala Pro Lys Arg Thr Gly
 1 5 10 15
 Trp Ala His Thr Thr Thr Pro Leu Thr Gly Pro Gln Arg Leu Gln Trp
 20 25 30
 Thr His Leu Pro Asp Ala Leu Tyr Pro Asp Val Ser Tyr Asp Leu Asp
 35 40 45
 Gly Cys Tyr Ser Gly Gly Ala Val Phe Ser Asp Gly Thr Leu Lys Leu
 50 55 60
 Phe Tyr Thr Gly Asn Arg Lys Ile Asp Gly Lys Arg Arg Ala Thr Gln
 65 70 75 80
 Asn Leu Val Glu Val Glu Asp Pro Thr Gly Leu Met Gly Gly Ile His
 85 90 95
 Arg Arg Ser Pro Lys Asn Pro Leu Ile Asp Gly Pro Ala Ser Gly Phe
 100 105 110
 Thr Pro His Tyr Arg Asp Pro Met Ile Ser Pro Asp Gly Asp Gly Trp
 115 120 125
 Lys Met Val Leu Gly Ala Gln Arg Glu Asn Leu Thr Gly Ala Ala Val
 130 135 140
 Leu Tyr Arg Ser Ala Asp Leu Glu Asn Trp Glu Phe Ser Gly Glu Ile
 145 150 155 160
 Thr Phe Asp Leu Ser Asp
 165

<210> 13
 <211> 479
 <212> DNA
 <213> Corynebacterium thermoaminogenes

<220>

<221> CDS

<222> (1)..(477)

<400> 13

lac lac cag cac gal cca ggt ttc ccc ttc gca cca aag cgc acc ggc 48
 Tyr Tyr Gln His Asp Pro Gly Phe Pro Phe Ala Pro Lys Arg Thr Gly
 1 5 10 15

1gg gct cac acc acc acg ccg ttg acc gga ccg cag cga ttg cag tgg 96
 Trp Ala His Thr Thr Thr Pro Leu Thr Gly Pro Gln Arg Leu Gln Trp
 20 25 30
 5 acg cac ctg ccc gac gct ctt tac ccg gat gca tcc tat gac ctg gat 144
 Thr His Leu Pro Asp Ala Leu Tyr Pro Asp Ala Ser Tyr Asp Leu Asp
 35 40 45
 10 gga tgc tat tcc ggt gga gcc gta ttt act gac ggc aca ctt aaa ctt 192
 Gly Cys Tyr Ser Gly Gly Ala Val Phe Thr Asp Gly Thr Leu Lys Leu
 50 55 60
 15 ttc tac acc ggc aac cta aaa att gac ggc aag cgc cgc gcc acc caa 240
 Phe Tyr Thr Gly Asn Leu Lys Ile Asp Gly Lys Arg Arg Ala Thr Gln
 65 70 75 80
 aac ctg gtc gaa gtc gag gac cca act ggg ctg atg ggc ggc att cat 288
 Asn Leu Val Glu Val Glu Asp Pro Thr Gly Leu Met Gly Gly Ile His
 85 90 95
 20 cgc cgt tgc cct aaa aat ccg ctt atc gac gga ccc gcc agc ggt ttc 336
 Arg Arg Ser Pro Lys Asn Pro Leu Ile Asp Gly Pro Ala Ser Gly Phe
 100 105 110
 25 aca ccc cat tac cgc gat ccc atg atc agc cct gat ggt gat ggt tgg 384
 Thr Pro His Tyr Arg Asp Pro Met Ile Ser Pro Asp Gly Asp Gly Trp
 115 120 125
 30 aaa atg gtt ctt ggg gcc caa cgc gaa aac ctg acc ggt gca gcg gtt 432
 Lys Met Val Leu Gly Ala Gln Arg Glu Asn Leu Thr Gly Ala Ala Val
 130 135 140
 cta tac cgc tgc aca gat ctt gaa aac tgg gaa ttc tcc ggt gaa at 479
 Leu Tyr Arg Ser Thr Asp Leu Glu Asn Trp Glu Phe Ser Gly Glu
 145 150 155
 35

<210> 14

<211> 159

<212> PRT

<213> Corynebacterium thermoaminogenes

<400> 14

45 Tyr Tyr Gln His Asp Pro Gly Phe Pro Phe Ala Pro Lys Arg Thr Gly
 1 5 10 15
 Trp Ala His Thr Thr Thr Pro Leu Thr Gly Pro Gln Arg Leu Gln Trp
 20 25 30
 50 Thr His Leu Pro Asp Ala Leu Tyr Pro Asp Ala Ser Tyr Asp Leu Asp
 35 40 45
 Gly Cys Tyr Ser Gly Gly Ala Val Phe Thr Asp Gly Thr Leu Lys Leu
 50 55 60
 55 Phe Tyr Thr Gly Asn Leu Lys Ile Asp Gly Lys Arg Arg Ala Thr Gln

65 70 75 80
 Asn Leu Val Glu Val Glu Asp Pro Thr Gly Leu Met Gly Gly Ile His
 85 90 95
 5 Arg Arg Ser Pro Lys Asn Pro Leu Ile Asp Gly Pro Ala Ser Gly Phe
 100 105 110
 Thr Pro His Tyr Arg Asp Pro Met Ile Ser Pro Asp Gly Asp Gly Trp
 115 120 125
 10 Lys Met Val Leu Gly Ala Gln Arg Glu Asn Leu Thr Gly Ala Ala Val
 130 135 140
 Leu Tyr Arg Ser Thr Asp Leu Glu Asn Trp Glu Phe Ser Gly Glu
 15 145 150 155

<210> 15

<211> 490

<212> DNA

<213> *Corynebacterium thermoaminogenes*

<400> 15

attttaatgg atattatcta tattttatca atattatcct taigcacctg aatggggacc 60
 25 aatgcatlgg ggacacgcac gtagtaaaga tttagttcat tgggaaacat taccgatlgc 120
 tttagaaccl ggagaigaag aagaaaaatg gtigtlttctc tggtaacaggt atagicaaag 180
 atgataagtl gtatttatit tatacaggtc accattaita taatgacgat gatcccgatc 240
 attttlggca aaatcaaaat atggcctata gigaagatgg caltcattit caaaaatata 300
 30 aacaaaaatgc aatcaliccl accccaccig aagataatc acalcacitc agagalccaa 360
 aggtatggga acatccatgg ctattaita catgatagta ggtagicaaa atgatagaga 420
 attaggacgt attatcttat atcgltctga ggaattatag aggggaatic tggtcctigag 480
 atcaatccaa 490

<210> 16

<211> 4254

<212> DNA

<213> *Corynebacterium thermoaminogenes*

<220>

<221> CDS

<222> (637).. (1362)

<220>

<221> CDS

<222> (1434).. (2315)

<220>

<221> CDS

<222> (2432).. (3115)

<220>

<221> CDS

<222> (3235)..(4065)

<400> 16

5
10
15
20
25
30
35
40
45
50
55

```

lcacggcgcg cagattaccc agtggccgt agagacgcig atcggcattc lcacgcaccg 60
cgcaggigti gaagacgatg agatcagggg tgcacccctc ccccgccgcg gtgtaaccgg 120
ccicctcgag cagaccggag agacgcctcg aatcgtggac gticacitgg cagccgaagg 180
tacgcacctc ataggigcgg gcagtggtgc ccicccggii ccccgccgcc gggaggggtg 240
cggcgggggtg gtccgggtgg gailgaltgg tglitacitg gtgggtalca atctgctgcg 300
lcacggggagg taatgtatc ggccgcgggc accctgacat aaacgtccga tccagaggaa 360
cgcaaccccg tggagtgtcg cagccatgca ggttgggcaa caccgtaacg gaacctagca 420
gagtggtagg attgacttca catcttttac ctattgagct attgataaaa tccgggcgga 480
aatggaaaat acccccacaa atcaccccaa ctgacctgig gaaagggcga gaaatccagg 540
gaaattcatt tcaaaatgga ctcaatcaca ggaattaccc cacaigacc aacattccit 600
tatgctaicc ccatgacgca gaccacaaat cacccg atg atc aag atg acg ggg 654
                                     Met Ile Lys Met Thr Gly
                                     1 5

gtg cag aag ttc ttc gat gac ttc cag gcc ctg acc gat atc aat ctt 702
Val Gln Lys Phe Phe Asp Asp Phe Gln Ala Leu Thr Asp Ile Asn Leu
                                     10 15 20

gag gtc ccc gcg gga cag gtc gti gti gti ctg gcc ccg tcc ggt tcc 750
Glu Val Pro Ala Gly Gln Val Val Val Val Leu Gly Pro Ser Gly Ser
                                     25 30 35

gga aag tcg acg ctg tgc cgc acc atc aac cgc ctg gaa acc atc gag 798
Gly Lys Ser Thr Leu Cys Arg Thr Ile Asn Arg Leu Glu Thr Ile Glu
                                     40 45 50

gag gga acc atc gag atc gat gga aaa ctg ctt ccg gag gag ggc aag 846
Glu Gly Thr Ile Glu Ile Asp Gly Lys Leu Leu Pro Glu Glu Gly Lys
                                     55 60 65 70

gac ctg gcc aag atc cgt gcc gac gtg ggc atg gtg ttc cag tct ttc 894
Asp Leu Ala Lys Ile Arg Ala Asp Val Gly Met Val Phe Gln Ser Phe
                                     75 80 85

aac ctg ttc ccc cac ctg acc atc aag gac aat gtc acc ctg ggc ccg 942
Asn Leu Phe Pro His Leu Thr Ile Lys Asp Asn Val Thr Leu Gly Pro
                                     90 95 100

atg aag gtc cgg aag atg aag aag tcc gag gcc aat gag gtg gcc atg 990
Met Lys Val Arg Lys Met Lys Lys Ser Glu Ala Asn Glu Val Ala Met
                                     105 110 115

aag ctg ttg gaa cgc gtc ggc atc gcc aac cag gcc gag aaa tac ccg 1038
Lys Leu Leu Glu Arg Val Gly Ile Ala Asn Gln Ala Glu Lys Tyr Pro
                                     120 125 130

gca cag ctg tcg ggc ggg cag cag cag cgc glg gcc atc gcc cgc gca 1086

```

Ala Gln Leu Ser Gly Gly Gln Gln Gln Arg Val Ala Ile Ala Arg Ala
 135 140 145 150
 5 ctc gcg atg aac ccc aag atc atg ctt ttc gac gaa cca acc tcc gcc 1134
 Leu Ala Met Asn Pro Lys Ile Met Leu Phe Asp Glu Pro Thr Ser Ala
 155 160 165
 10 ctc gac ccc gag atg gtc aac gag gtt ctg gac gtc atg gcg agt ctg 1182
 Leu Asp Pro Glu Met Val Asn Glu Val Leu Asp Val Met Ala Ser Leu
 170 175 180
 gcc aag gaa ggc atg acc atg gtg tgt gtc acc cac gag atg ggt ttc 1230
 Ala Lys Glu Gly Met Thr Met Val Cys Val Thr His Glu Met Gly Phe
 185 190 195
 15 gca cgc agg gcc gca gac cgt gtg ctg ttc atg tct gac ggc gcc atc 1278
 Ala Arg Arg Ala Ala Asp Arg Val Leu Phe Met Ser Asp Gly Ala Ile
 200 205 210
 20 gtc gag gac tcc gac ccg gag acc ttc ttc acc aat cca caa acc gac 1326
 Val Glu Asp Ser Asp Pro Glu Thr Phe Phe Thr Asn Pro Gln Thr Asp
 215 220 225 230
 cgg gcg aag gat ttc ctg ggc aag atc ctc gcc cac tgacctcccc 1372
 25 Arg Ala Lys Asp Phe Leu Gly Lys Ile Leu Ala His
 235 240
 tcactctgtg tccaactccc ccgcgtggcca aaatcagcga ccatgacca caggagcalt 1432
 a atg tgc cac aaa cgc atg ttc acc cgt ctc gcc gca gcc acc agc gca 1481
 30 Met Ser His Lys Arg Met Phe Thr Arg Leu Ala Ala Thr Ser Ala
 245 250 255
 gct gtt ctc gcc ggc atc acc ctc acc gcc tgt ggt gat tcc gag ggt 1529
 Ala Val Leu Ala Gly Ile Thr Leu Thr Ala Cys Gly Asp Ser Glu Gly
 260 265 270
 35 ggt gac ggt ctg ctc gcc gcc atc gaa aat ggc aat gtc acc atc ggc 1577
 Gly Asp Gly Leu Leu Ala Ala Ile Glu Asn Gly Asn Val Thr Ile Gly
 275 280 285 290
 40 acc aag tac gat cag ccg ggt ctg gga ctg cgt aac ccg gac aat tcc 1625
 Thr Lys Tyr Asp Gln Pro Gly Leu Gly Leu Arg Asn Pro Asp Asn Ser
 295 300 305
 atg agc gga ctg gat gtc gac gtc gcg cag tac gtg gtc aac tcc atc 1673
 45 Met Ser Gly Leu Asp Val Asp Val Ala Gln Tyr Val Val Asn Ser Ile
 310 315 320
 gcc gat gac aac ggt tgg gat cac ccc acc gtg gaa tgg cgc gag acc 1721
 Ala Asp Asp Asn Gly Trp Asp His Pro Thr Val Glu Trp Arg Glu Thr
 325 330 335
 50 ccc tcc gcc cag cgc gag acc ctc atc cag aac ggt gag gtc gat atg 1769
 Pro Ser Ala Gln Arg Glu Thr Leu Ile Gln Asn Gly Glu Val Asp Met
 340 345 350
 55 atc gcc gca acc tac tcc atc aac ccc gga cgc tcc gaa tgc gtg aac 1817

• 55

Ser Ala Ile Gly Ser Met Ile Leu Gly Thr Ile Leu Thr Ala Met Arg
 565 570 575
 5 gig tcc ccg gig aag atc ctg cgc agc ata tcc acc gcc tac atc aac 2602
 Val Ser Pro Val Lys Ile Leu Arg Ser Ile Ser Thr Ala Tyr Ile Asn
 580 585 590
 10 acg gtc cgt aac acc cca ctg acc ctg gig atc ctg ttc tgt tcc ttc 2650
 Thr Val Arg Asn Thr Pro Leu Thr Leu Val Ile Leu Phe Cys Ser Phe
 595 600 605
 ggc ctg tat cag aat ctc ggt ctc acc ctc gcc ggt cgc gac agt tcc 2698
 Gly Leu Tyr Gln Asn Leu Gly Leu Thr Leu Ala Gly Arg Asp Ser Ser
 15 610 615 620 625
 acc ttt ctg gcc gat aac aac ttc cgg ctc gcg gtg ctc gga ttc atc 2746
 Thr Phe Leu Ala Asp Asn Asn Phe Arg Leu Ala Val Leu Gly Phe Ile
 630 635 640
 20 ctg tac acc tcc gcc ttc gtt gcg gaa tca ctc cgg tca gcc atc aac 2794
 Leu Tyr Thr Ser Ala Phe Val Ala Glu Ser Leu Arg Ser Gly Ile Asn
 645 650 655
 acc gig cac ttc ggg cag gcg gag gcc gcc cgg tcc ctg gga ctc ggt 2842
 Thr Val His Phe Gly Gln Ala Glu Ala Ala Arg Ser Leu Gly Leu Gly
 25 660 665 670
 ttc agt gac atc ttc cgg tcc atc atc ttc ccc cag gcg gig cgt gcc 2890
 Phe Ser Asp Ile Phe Arg Ser Ile Ile Phe Pro Gln Ala Val Arg Ala
 30 675 680 685
 gcc atc atc ccg ctg ggc aac acc ctc atc gcc ctg acc aag aac acc 2938
 Ala Ile Ile Pro Leu Gly Asn Thr Leu Ile Ala Leu Thr Lys Asn Thr
 690 695 700 705
 35 acg atc gcg tcc gig atc ggc gtc ggt gag gcc tcc ctg ctg atg aag 2986
 Thr Ile Ala Ser Val Ile Gly Val Gly Glu Ala Ser Leu Leu Met Lys
 710 715 720
 40 tcc acg att gaa aat cat gcc aac atg ctc ttc gtc gig ttc gcc atc 3034
 Ser Thr Ile Glu Asn His Ala Asn Met Leu Phe Val Val Phe Ala Ile
 725 730 735
 ttc gcc gtc ggc ttc atg atc ctc acc ctc ccc atg ggc ctg ggg ctt 3082
 Phe Ala Val Gly Phe Met Ile Leu Thr Leu Pro Met Gly Leu Gly Leu
 45 740 745 750
 gga aaa ctc gct gag aaa atg gcg gig aag aaa taatgtccctc ctccgtacgc 3135
 Gly Lys Leu Ala Glu Lys Met Ala Val Lys Lys
 755 760
 50 gcaacagtcctc tctacgacgc ccccgcccc cggggacgca ggltcaaacac catcatcacc 3195
 atcgcaccca cccgtgtggc agtggccgtc cigtctgg gig ggc agt gtt ctc 3249
 Val Gly Ser Val Leu
 765
 55 cag gaa aac ggc cag ttg gac ggc gac aaa tgg acc ccg ttc ctc gat 3297

| | Gln | Glu | Asn | Gly | Gln | Leu | Asp | Gly | Asp | Lys | Trp | Thr | Pro | Phe | Leu | Asp | |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| | 770 | | | | | 775 | | | | | 780 | | | | | 785 | |
| 5 | ccc | cag | acc | igg | acc | acc | tat | ctt | ctg | ccc | ggc | ctg | igg | gga | acc | ctg | 3345 |
| | Pro | Gln | Thr | Trp | Thr | Thr | Tyr | Leu | Leu | Pro | Gly | Leu | Trp | Gly | Thr | Leu | |
| | | | | | 790 | | | | | 795 | | | | | 800 | | |
| 10 | aag | gca | gcg | gig | gcc | tcc | atc | ctt | ctc | gcg | ctg | atc | atg | ggc | acc | ctg | 3393 |
| | Lys | Ala | Ala | Val | Ala | Ser | Ile | Leu | Leu | Ala | Leu | Ile | Met | Gly | Thr | Leu | |
| | | | | 805 | | | | | | 810 | | | | | 815 | | |
| 15 | ctc | ggg | ctc | gga | cgc | atc | tcc | gaa | atc | cgg | ctc | ctg | cgc | igg | ttc | tgc | 3441 |
| | Leu | Gly | Leu | Gly | Arg | Ile | Ser | Glu | Ile | Arg | Leu | Leu | Arg | Trp | Phe | Cys | |
| | | | | 820 | | | | | 825 | | | | 830 | | | | |
| 20 | ggg | atc | atc | atc | gag | acc | ttc | cgt | gcc | atc | cgg | gtg | ctg | atc | ctc | atg | 3489 |
| | Gly | Ile | Ile | Ile | Glu | Thr | Phe | Arg | Ala | Ile | Pro | Val | Leu | Ile | Leu | Met | |
| | | 835 | | | | | 840 | | | | 845 | | | | | | |
| 25 | atc | ttc | gcc | tat | cag | tig | ttc | gcc | cgt | tac | cag | ctc | gtt | cca | tca | cgc | 3537 |
| | Ile | Phe | Ala | Tyr | Gln | Leu | Phe | Ala | Arg | Tyr | Gln | Leu | Val | Pro | Ser | Arg | |
| | 850 | | | | 855 | | | | | 860 | | | | | 865 | | |
| 30 | cag | ctg | gcc | ttc | gcc | gcg | gig | gtc | ttc | ggt | ctc | acc | atg | tac | aac | ggc | 3585 |
| | Gln | Leu | Ala | Phe | Ala | Ala | Val | Val | Phe | Gly | Leu | Thr | Met | Tyr | Asn | Gly | |
| | | | | 870 | | | | | 875 | | | | | 880 | | | |
| 35 | tcc | gtc | atc | gcc | gag | atc | ctt | aga | tcc | ggt | atc | gcc | tcc | ctg | cgg | aag | 3633 |
| | Ser | Val | Ile | Ala | Glu | Ile | Leu | Arg | Ser | Gly | Ile | Ala | Ser | Leu | Pro | Lys | |
| | | | | 885 | | | | | 890 | | | | 895 | | | | |
| 40 | gga | cag | cgt | gag | gcg | gcg | atc | gcc | ctg | ggc | atg | tca | acc | cgc | cag | acc | 3681 |
| | Gly | Gln | Arg | Glu | Ala | Ala | Ile | Ala | Leu | Gly | Met | Ser | Thr | Arg | Gln | Thr | |
| | | 900 | | | | | | 905 | | | | | 910 | | | | |
| 45 | acc | igg | tcc | atc | ctg | ctc | ccc | cag | gcg | gig | gca | gcg | atg | ctg | ccc | gcc | 3729 |
| | Thr | Trp | Ser | Ile | Leu | Leu | Pro | Gln | Ala | Val | Ala | Ala | Met | Leu | Pro | Ala | |
| | | 915 | | | | | 920 | | | | | 925 | | | | | |
| 50 | ctg | atc | gcg | cag | atg | gtc | atc | gcg | ctg | aag | gac | tcc | gcc | ctc | ggt | tac | 3777 |
| | Leu | Ile | Ala | Gln | Met | Val | Ile | Ala | Leu | Lys | Asp | Ser | Ala | Leu | Gly | Tyr | |
| | 930 | | | | 935 | | | | | 940 | | | | 945 | | | |
| 55 | cag | atc | ggt | tat | atc | gag | gig | gta | cgc | tcc | ggt | atc | cag | tcc | gca | tcc | 3825 |
| | Gln | Ile | Gly | Tyr | Ile | Glu | Val | Val | Arg | Ser | Gly | Ile | Gln | Ser | Ala | Ser | |
| | | | | 950 | | | | | 955 | | | | | 960 | | | |
| 60 | gtc | aac | cgg | aac | tac | ctg | gct | gcc | ctc | gcg | gig | gtc | gcg | gtc | atc | atg | 3873 |
| | Val | Asn | Arg | Asn | Tyr | Leu | Ala | Ala | Leu | Ala | Val | Val | Ala | Val | Ile | Met | |
| | | | | 965 | | | | 970 | | | | | 975 | | | | |
| 65 | atc | ctg | atc | aac | ttc | gca | ctg | acc | gca | ctg | gca | gag | cgt | atc | cag | cgt | 3921 |
| | Ile | Leu | Ile | Asn | Phe | Ala | Leu | Thr | Ala | Leu | Ala | Glu | Arg | Ile | Gln | Arg | |
| | | 980 | | | | | 985 | | | | | 990 | | | | | |
| 70 | cag | ctg | cgt | gcc | gga | cgt | gcc | cgc | agg | aac | att | gtg | gca | aag | gtg | ccc | 3969 |
| | Gln | Leu | Arg | Ala | Gly | Arg | Ala | Arg | Arg | Asn | Ile | Val | Ala | Lys | Val | Pro | |

995 1000 1005
 gag gaa ccc gat cag ggc ctg gat acc aag gac aat gtg aac gtg gat 4017
 Glu.Glu Pro Asp Gln Gly Leu Asp Thr Lys Asp Asn Val Asn Val Asp
 1010 1015 1020 1025
 tgg cac gat ccc gat tac aag gaa gtc aaa cac ccg gga ccg tca ttc 4065
 Trp His Asp Pro Asp Tyr Lys Glu Val Lys His Pro Gly Pro Ser Phe
 1030 1035 1040
 tgacaggctc ctggatcccc gctgcgggtc ggaggcgggt gcaacaatga agtccggctg 4125
 cccagatgtc tggggcagcc ggactttgtg gcagatcaat gctgactgag gtcctcgaig 4185
 cgtcatcga gagcctcccg ggccaggctc atcgacatac ccgcggggaa tccacgacgg 4245
 gcaaglgct 4254

 <210> 17
 <211> 242
 <212> PRT
 <213> *Corynebacterium thermoaminogenes*

 <400> 17
 Met Ile Lys Met Thr Gly Val Gln Lys Phe Phe Asp Asp Phe Gln Ala
 1 5 10 15
 Leu Thr Asp Ile Asn Leu Glu Val Pro Ala Gly Gln Val Val Val Val
 20 25 30
 Leu Gly Pro Ser Gly Ser Gly Lys Ser Thr Leu Cys Arg Thr Ile Asn
 35 40 45
 Arg Leu Glu Thr Ile Glu Glu Gly Thr Ile Glu Ile Asp Gly Lys Leu
 50 55 60
 Leu Pro Glu Glu Gly Lys Asp Leu Ala Lys Ile Arg Ala Asp Val Gly
 65 70 75 80
 Met Val Phe Gln Ser Phe Asn Leu Phe Pro His Leu Thr Ile Lys Asp
 85 90 95
 Asn Val Thr Leu Gly Pro Met Lys Val Arg Lys Met Lys Lys Ser Glu
 100 105 110
 Ala Asn Glu Val Ala Met Lys Leu Glu Arg Val Gly Ile Ala Asn
 115 120 125
 Gln Ala Glu Lys Tyr Pro Ala Gln Leu Ser Gly Gly Gln Gln Gln Arg
 130 135 140
 Val Ala Ile Ala Arg Ala Leu Ala Met Asn Pro Lys Ile Met Leu Phe
 145 150 155 160
 Asp Glu Pro Thr Ser Ala Leu Asp Pro Glu Met Val Asn Glu Val Leu
 165 170 175
 Asp Val Met Ala Ser Leu Ala Lys Glu Gly Met Thr Met Val Cys Val
 180 185 190
 Thr His Glu Met Gly Phe Ala Arg Arg Ala Ala Asp Arg Val Leu Phe

195 200 205
 Met Ser Asp Gly Ala Ile Val Glu Asp Ser Asp Pro Glu Thr Phe Phe
 210 215 220
 5 Thr Asn Pro Gln Thr Asp Arg Ala Lys Asp Phe Leu Gly Lys Ile Leu
 225 230 235 240
 Ala His
 10
 <210> 18
 <211> 294
 <212> PRT
 15 <213> *Corynebacterium thermoaminogenes*
 <400> 18
 Met Ser His Lys Arg Met Phe Thr Arg Leu Ala Ala Ala Thr Ser Ala
 20 1 5 10 15
 Ala Val Leu Ala Gly Ile Thr Leu Thr Ala Cys Gly Asp Ser Glu Gly
 20 25 30
 Gly Asp Gly Leu Leu Ala Ala Ile Glu Asn Gly Asn Val Thr Ile Gly
 25 35 40 45
 Thr Lys Tyr Asp Gln Pro Gly Leu Gly Leu Arg Asn Pro Asp Asn Ser
 50 55 60
 Met Ser Gly Leu Asp Val Asp Val Ala Gln Tyr Val Val Asn Ser Ile
 30 65 70 75 80
 Ala Asp Asp Asn Gly Trp Asp His Pro Thr Val Glu Trp Arg Glu Thr
 85 90 95
 Pro Ser Ala Gln Arg Glu Thr Leu Ile Gln Asn Gly Glu Val Asp Met
 35 100 105 110
 Ile Ala Ala Thr Tyr Ser Ile Asn Pro Gly Arg Ser Glu Ser Val Asn
 115 120 125
 Phe Gly Gly Pro Tyr Leu Leu Thr His Gln Ala Leu Leu Val Arg Glu
 40 130 135 140
 Asp Asp Asp Arg Ile Gln Thr Leu Glu Asp Leu Asp Asp Gly Leu Ile
 145 150 155 160
 Leu Cys Ser Val Thr Gly Ser Thr Pro Ala Gln Lys Val Lys Asp Val
 45 165 170 175
 Leu Pro Gly Val Gln Leu Gln Glu Tyr Asp Thr Tyr Ser Ser Cys Val
 180 185 190
 Glu Ala Leu Ser Gln Gly Asn Val Asp Ala Met Thr Thr Asp Ala Thr
 50 195 200 205
 Ile Leu Phe Gly Tyr Ala Gln Gln Arg Glu Gly Glu Phe Arg Val Val
 210 215 220
 Glu Met Glu Gln Asp Gly Glu Pro Phe Thr Asn Glu Tyr Tyr Gly Ile
 55 225 230 235 240

Gly Ile Thr Lys Asp Asp Thr Glu Ala Thr Asp Ala Ile Asn Ala Ala
 245 250 255
 5 Leu Glu Arg Met Tyr Ala Asp Gly Ser Phe Gln Arg Phe Leu Thr Glu
 260 265 270
 Asn Leu Gly Glu Asp Ser Gln Val Val Gln Glu Gly Thr Pro Gly Asp
 275 280 285
 10 Leu Ser Phe Leu Asp Glu
 290

<210> 19

15 <211> 228

<212> PRT

<213> *Corynebacterium thermoaminogenes*

20 <400> 19

Met Ser Thr Leu Trp Ala Asp Leu Gly Pro Ser Leu Leu Pro Ala Phe
 1 5 10 15
 Trp Val Thr Ile Gln Leu Thr Val Tyr Ser Ala Ile Gly Ser Met Ile
 20 25 30
 25 Leu Gly Thr Ile Leu Thr Ala Met Arg Val Ser Pro Val Lys Ile Leu
 35 40 45
 Arg Ser Ile Ser Thr Ala Tyr Ile Asn Thr Val Arg Asn Thr Pro Leu
 50 55 60
 Thr Leu Val Ile Leu Phe Cys Ser Phe Gly Leu Tyr Gln Asn Leu Gly
 65 70 75 80
 Leu Thr Leu Ala Gly Arg Asp Ser Ser Thr Phe Leu Ala Asp Asn Asn
 85 90 95
 35 Phe Arg Leu Ala Val Leu Gly Phe Ile Leu Tyr Thr Ser Ala Phe Val
 100 105 110
 Ala Glu Ser Leu Arg Ser Gly Ile Asn Thr Val His Phe Gly Gln Ala
 115 120 125
 40 Glu Ala Ala Arg Ser Leu Gly Leu Gly Phe Ser Asp Ile Phe Arg Ser
 130 135 140
 Ile Ile Phe Pro Gln Ala Val Arg Ala Ala Ile Ile Pro Leu Gly Asn
 145 150 155 160
 Thr Leu Ile Ala Leu Thr Lys Asn Thr Thr Ile Ala Ser Val Ile Gly
 165 170 175
 Val Gly Glu Ala Ser Leu Leu Met Lys Ser Thr Ile Glu Asn His Ala
 180 185 190
 50 Asn Met Leu Phe Val Val Phe Ala Ile Phe Ala Val Gly Phe Met Ile
 195 200 205
 Leu Thr Leu Pro Met Gly Leu Gly Leu Gly Lys Leu Ala Glu Lys Met
 210 215 220
 55

Ala Val Lys Lys

225

<210> 20

<211> 277

<212> PRT

<213> Corynebacterium thermoaminogenes

<400> 20

Val Gly Ser Val Leu Gln Glu Asn Gly Gln Leu Asp Gly Asp Lys Trp

1 5 10 15

Thr Pro Phe Leu Asp Pro Gln Thr Trp Thr Thr Tyr Leu Leu Pro Gly

20 25 30

Leu Trp Gly Thr Leu Lys Ala Ala Val Ala Ser Ile Leu Leu Ala Leu

35 40 45

Ile Met Gly Thr Leu Leu Gly Leu Gly Arg Ile Ser Glu Ile Arg Leu

50 55 60

Leu Arg Trp Phe Cys Gly Ile Ile Ile Glu Thr Phe Arg Ala Ile Pro

65 70 75 80

Val Leu Ile Leu Met Ile Phe Ala Tyr Gln Leu Phe Ala Arg Tyr Gln

85 90 95

Leu Val Pro Ser Arg Gln Leu Ala Phe Ala Ala Val Val Phe Gly Leu

100 105 110

Thr Met Tyr Asn Gly Ser Val Ile Ala Glu Ile Leu Arg Ser Gly Ile

115 120 125

Ala Ser Leu Pro Lys Gly Gln Arg Glu Ala Ala Ile Ala Leu Gly Met

130 135 140

Ser Thr Arg Gln Thr Thr Trp Ser Ile Leu Leu Pro Gln Ala Val Ala

145 150 155 160

Ala Met Leu Pro Ala Leu Ile Ala Gln Met Val Ile Ala Leu Lys Asp

165 170 175

Ser Ala Leu Gly Tyr Gln Ile Gly Tyr Ile Glu Val Val Arg Ser Gly

180 185 190

Ile Gln Ser Ala Ser Val Asn Arg Asn Tyr Leu Ala Ala Leu Ala Val

195 200 205

Val Ala Val Ile Met Ile Leu Ile Asn Phe Ala Leu Thr Ala Leu Ala

210 215 220

Glu Arg Ile Gln Arg Gln Leu Arg Ala Gly Arg Ala Arg Arg Asn Ile

225 230 235 240

Val Ala Lys Val Pro Glu Glu Pro Asp Gln Gly Leu Asp Thr Lys Asp

245 250 255

Asn Val Asn Val Asp Trp His Asp Pro Asp Tyr Lys Glu Val Lys His

260 265 270

Pro Gly Pro Ser Phe

275

5

<210> 21

<211> 3598

<212> DNA

10

<213> Corynebacterium thermoaminogenes

<220>

<221> CDS

<222> (454)..(3222)

15

<400> 21

agcacggcca aacatgagag aaacttcaca ttitgaattt cccctttcct gcatalggaa 60
 aaccgccggg gacaccccg ccatitgggc agtcccccc acccaccat gtcacattt 120
 tccataatgt ggccgtgaac acccttgggc tcaaggctc cagccccac cgggacccctc 180
 atcagcaggt gaaacagacc ctctgcaat gctitgttaa aaagaaccgc cctitgtgcg 240
 tatctitgtg tcaatitgtc gcgcacigcc accagcttct ctccagatgt aacacggctc 300
 ggaaatccct cccggalacc ctgcacgccc caccctccac accgacaccg gcggggagggt 360
 ccgggcacgt tticagctgc gggatgagga agcggctgcc ggtccccgg tgcataaac 420
 gaaatgaaaa acattccaac aggagggtgt gaa atg gcc gat caa gca aaa ctt 474

Met Ala Asp Gln Ala Lys Leu

1

5

30

ggt ggc aaa ccc aca gat gac acc aac ttc gcg atg atc cgt gat ggc 522
 Gly Gly Lys Pro Thr Asp Asp Thr Asn Phe Ala Met Ile Arg Asp Gly

10

15

20

35

gtt gca tct tat ttg aac gac tcc gac ccg gag gag acc aag gag tgg 570
 Val Ala Ser Tyr Leu Asn Asp Ser Asp Pro Glu Glu Thr Lys Glu Trp

25

30

35

40

atg gac tcc cta gac ggt cta ctg cag gat tcc tct ccg gag cgc gcc 618
 Met Asp Ser Leu Asp Gly Leu Leu Gln Asp Ser Ser Pro Glu Arg Ala

40

45

50

55

cgt tac ctg atg ctg cgc ctg ctg gag cgg gca tcc gcc aag cgt gtc 666
 Arg Tyr Leu Met Leu Arg Leu Leu Glu Arg Ala Ser Ala Lys Arg Val

60

65

70

45

cca ctg ccc ccg atg acg tcc acc gat tac gtc aac acc atc ccc aca 714
 Pro Leu Pro Pro Met Thr Ser Thr Asp Tyr Val Asn Thr Ile Pro Thr

75

80

85

50

tcc atg gag ccc gat ttc ccg ggt gat gag gag atg gag aag cgc tac 762
 Ser Met Glu Pro Asp Phe Pro Gly Asp Glu Glu Met Glu Lys Arg Tyr

90

95

100

cgc cgc tgg atg cgc tgg aac gcc gcc atc atg gtg cac cgt gcc cag 810
 Arg Arg Trp Met Arg Trp Asn Ala Ala Ile Met Val His Arg Ala Gln

105

110

115

55

cgc ccg gga atc ggt gtg ggt ggg cac atc tcc acc tac gcc ggc gcc 858

4)

55

| | | | | |
|----|---|-----|-----|------|
| | 345 | 350 | 355 | |
| | cac ttc ttc ggc cgt gac ccc cgc acc ctc aag ctc gtc gag gac atg | | | 1578 |
| 5 | His Phe Phe Gly Arg Asp Pro Arg Thr Leu Lys Leu Val Glu Asp Met | | | |
| | 360 | 365 | 370 | 375 |
| | acc gac gag gag atc tgg aag ctg ccc cgt ggt ggc cal gac tac cgt | | | 1626 |
| | Thr Asp Glu Glu Ile Trp Lys Leu Pro Arg Gly Gly His Asp Tyr Arg | | | |
| 10 | | 380 | 385 | 390 |
| | aag gtc tac gcc gcc tac aag cgt gcg ctg gag acc aag gac cgc ccg | | | 1674 |
| | Lys Val Tyr Ala Ala Tyr Lys Arg Ala Leu Glu Thr Lys Asp Arg Pro | | | |
| | 395 | 400 | 405 | |
| 15 | acc gtc att ctc gcc cal acc atc aag ggc tac ggc ctg ggc cac aac | | | 1722 |
| | Thr Val Ile Leu Ala His Thr Ile Lys Gly Tyr Gly Leu Gly His Asn | | | |
| | 410 | 415 | 420 | |
| | ttc gag ggc cgc aac gcg acc cac cag atg aag aag ctg acc ctg gat | | | 1770 |
| 20 | Phe Glu Gly Arg Asn Ala Thr His Gln Met Lys Lys Leu Thr Leu Asp | | | |
| | 425 | 430 | 435 | |
| | gac ctg aag ctg ttc cgt gac aag cag ggt ctg ccc atc acc gat gag | | | 1818 |
| | Asp Leu Lys Leu Phe Arg Asp Lys Gln Gly Leu Pro Ile Thr Asp Glu | | | |
| 25 | 440 | 445 | 450 | 455 |
| | gag ctg gag aag gat ccc tac ctg cct ccg tac tac cac ccg ggt gag | | | 1866 |
| | Glu Leu Glu Lys Asp Pro Tyr Leu Pro Pro Tyr Tyr His Pro Gly Glu | | | |
| | 460 | 465 | 470 | |
| 30 | gac gca ccg gag atc aag tac atg aag gag cgt cgc cag gcg ctc ggt | | | 1914 |
| | Asp Ala Pro Glu Ile Lys Tyr Met Lys Glu Arg Arg Gln Ala Leu Gly | | | |
| | 475 | 480 | 485 | |
| | ggt ttc ctg ccg gag cgc cgt gag aag tac gag cca ctg cag gtt ccc | | | 1962 |
| 35 | Gly Phe Leu Pro Glu Arg Arg Glu Lys Tyr Glu Pro Leu Gln Val Pro | | | |
| | 490 | 495 | 500 | |
| | ccg ctg gac aag ctg cgg tcc gtg cgc aag ggt tcc ggc aag cag cag | | | 2010 |
| | Pro Leu Asp Lys Leu Arg Ser Val Arg Lys Gly Ser Gly Lys Gln Gln | | | |
| 40 | 505 | 510 | 515 | |
| | gtg gcc acc acc atg gcc acg gtg cgt acc ttc aag gaa ctc atg cgg | | | 2058 |
| | Val Ala Thr Thr Met Ala Thr Val Arg Thr Phe Lys Glu Leu Met Arg | | | |
| | 520 | 525 | 530 | 535 |
| 45 | gac aag aac ctg gcc gac cgc ttg gtc ccg atc atc ccg gat gag gcc | | | 2106 |
| | Asp Lys Asn Leu Ala Asp Arg Leu Val Pro Ile Ile Pro Asp Glu Ala | | | |
| | 540 | 545 | 550 | |
| | cgc acc ttc ggc ctg gac tcc tgg ttc ccg acc ctg aaa atc tac aac | | | 2154 |
| 50 | Arg Thr Phe Gly Leu Asp Ser Trp Phe Pro Thr Leu Lys Ile Tyr Asn | | | |
| | 555 | 560 | 565 | |
| | ccg cac ggt cag aac tac gtg ccg gtc gac cal gac ctc atg ctg tcc | | | 2202 |
| | Pro His Gly Gln Asn Tyr Val Pro Val Asp His Asp Leu Met Leu Ser | | | |
| 55 | 570 | 575 | 580 | |

| | | |
|----|---|------|
| | lac cgl gag gcc aag gac ggc cag atc clg cal gag ggc atc aac gag | 2250 |
| | Tyr Arg Glu Ala Lys Asp Gly Gln Ile Leu His Glu Gly Ile Asn Glu | |
| 5 | 585 590 595 | |
| | gcc ggt tcc gtg gca tgc ttt atc gcc gcc gga acc tcc lac gcc acc | 2298 |
| | Ala Gly Ser Val Ala Ser Phe Ile Ala Ala Gly Thr Ser Tyr Ala Thr | |
| | 600 605 610 615 | |
| 10 | cat ggc gag gcc atg atc ccg clg lac atc ttc lac tgc atg ttc ggc | 2346 |
| | His Gly Glu Ala Met Ile Pro Leu Tyr Ile Phe Tyr Ser Met Phe Gly | |
| | 620 625 630 | |
| | ttc cag cgc acc ggt gac ggc atc tgg gcc gca gcc gac cag atg acg | 2394 |
| 15 | Phe Gln Arg Thr Gly Asp Gly Ile Trp Ala Ala Ala Asp Gln Met Thr | |
| | 635 640 645 | |
| | cgt ggt ttc ctc clg ggc gcc acc gcc ggt cgc acc acc clg acc ggt | 2442 |
| | Arg Gly Phe Leu Leu Gly Ala Thr Ala Gly Arg Thr Thr Leu Thr Gly | |
| 20 | 650 655 660 | |
| | gag gcc ctc cag cac atg gat ggc cac tcc ccg atc clg gcc tcc acc | 2490 |
| | Glu Gly Leu Gln His Met Asp Gly His Ser Pro Ile Leu Ala Ser Thr | |
| | 665 670 675 | |
| 25 | aac ccc ggt gtg gag acc tat gac ccg gcg ttc tcc lac gag atc gcg | 2538 |
| | Asn Pro Gly Val Glu Thr Tyr Asp Pro Ala Phe Ser Tyr Glu Ile Ala | |
| | 680 685 690 695 | |
| | cac clg gtc cac cgc ggc atc gac cgc atg tac gga ccg ggc aag ggt | 2586 |
| 30 | His Leu Val His Arg Gly Ile Asp Arg Met Tyr Gly Pro Gly Lys Gly | |
| | 700 705 710 | |
| | gag aat gtc atc tac ttc acc atc lac aac gag cca acc ccg cag | 2634 |
| | Glu Asn Val Ile Tyr Tyr Leu Thr Ile Tyr Asn Glu Pro Thr Pro Gln | |
| 35 | 715 720 725 | |
| | ccg gct gag cct gag gat clg gac gtc gag ggc clg cac aag ggc atc | 2682 |
| | Pro Ala Glu Pro Glu Asp Leu Asp Val Glu Gly Leu His Lys Gly Ile | |
| | 730 735 740 | |
| 40 | lac ctc lac gac aag gcc gcc gag ggt gag ggc cal gag gcc tgc atc | 2730 |
| | Tyr Leu Tyr Asp Lys Ala Ala Glu Gly Glu Gly His Glu Ala Ser Ile | |
| | 745 750 755 | |
| | clg gcc tcc ggc atc ggc atg cag tgg gca clg cgc gcc cgt gac atc | 2778 |
| 45 | Leu Ala Ser Gly Ile Gly Met Gln Trp Ala Leu Arg Ala Arg Asp Ile | |
| | 760 765 770 775 | |
| | ctc gcc gag gat tac ggc atc cgt gcc aac atc ttc tcc gcc acc tgc | 2826 |
| | Leu Ala Glu Asp Tyr Gly Ile Arg Ala Asn Ile Phe Ser Ala Thr Ser | |
| 50 | 780 785 790 | |
| | tgg gtg gag clg gcc cgc gac ggt gcc cgc cgt aac clg gag gcg clg | 2874 |
| | Trp Val Glu Leu Ala Arg Asp Gly Ala Arg Arg Asn Leu Glu Ala Leu | |
| | 795 800 805 | |
| 55 | cgc aac ccg ggt gcg gat gtc ggt gag gca ttc gtg acc acc cag clg | 2922 |

Arg Asn Pro Gly Ala Asp Val Gly Glu Ala Phe Val Thr Thr Gln Leu
 810 815 820
 5 aag aag ggt tcc ggc ccc tac gtc gcg glg tcc gac ttc gcg acc gac 2970
 Lys Lys Gly Ser Gly Pro Tyr Val Ala Val Ser Asp Phe Ala Thr Asp
 825 830 835
 10 ctg ccg aac cag atc cgc gag tgg gtt ccc ggt gac tac atc gtc ctc 3018
 Leu Pro Asn Gln Ile Arg Glu Trp Val Pro Gly Asp Tyr Ile Val Leu
 840 845 850 855
 ggt gcc gac ggc ttc ggt ttc tcc gat acc cgt ccg gca gcc cgt cgt 3066
 Gly Ala Asp Gly Phe Gly Phe Ser Asp Thr Arg Pro Ala Ala Arg Arg
 15 860 865 870
 tac ttc aac atc gac gcc gag tcc atc gtc glg gcg gtc ctg cgc ggc 3114
 Tyr Phe Asn Ile Asp Ala Glu Ser Ile Val Val Ala Val Leu Arg Gly
 875 880 885
 20 ctg gtc cgc gag ggt gtc atc gat gcc tcc glg gcg gcg cac gcg gct 3162
 Leu Val Arg Glu Gly Val Ile Asp Ala Ser Val Ala Ala His Ala Ala
 890 895 900
 gag aag tac aag ctg tcc gac ccg acg gca cca cag gtc gat ccg gac 3210
 25 Glu Lys Tyr Lys Leu Ser Asp Pro Thr Ala Pro Gln Val Asp Pro Asp
 905 910 915
 gca ccg atc gag tagaccigt tgcgcagaa aaacaccccc gcccccctcac 3262
 Ala Pro Ile Glu
 30 920
 atgatgaggg gggcgggggt gtcctcggtt acggcgggla caggggggla tcagcccagc 3322
 atgccttat cggagagcgt cgcgcccttg atcttggcga atcttcgcag cagatcccgc 3382
 acggtagagct tctgcttcac ctctgcgcgt gccctataga cgaaccgicc ctctgtcctc 3442
 35 atgatgaggc gggtaccag gcggaatagcc tcttccatgt tctgggtgac catgaggggtg 3502
 gtcagtttgc cgtcttcgac gatcttctcg gtcaggggtg tgaccagttc ggtctgcctg 3562
 gggctccaggg cggcgggtgt ttcgtcgaga agcatg 3598
 40 <210> 22
 <211> 923
 <212> PRT
 <213> Corynebacterium thermoaminogenes
 45
 <400> 22
 Met Ala Asp Gln Ala Lys Leu Gly Gly Lys Pro Thr Asp Asp Thr Asn
 1 5 10 15
 50 Phe Ala Met Ile Arg Asp Gly Val Ala Ser Tyr Leu Asn Asp Ser Asp
 20 25 30
 Pro Glu Glu Thr Lys Glu Trp Met Asp Ser Leu Asp Gly Leu Leu Gln
 35 40 45
 55 Asp Ser Ser Pro Glu Arg Ala Arg Tyr Leu Met Leu Arg Leu Leu Glu

| | | | | | | | | | | | | | | | | |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| | 50 | | 55 | | 60 | | | | | | | | | | | |
| | Arg | Ala | Ser | Ala | Lys | Arg | Val | Pro | Leu | Pro | Pro | Met | Thr | Ser | Thr | Asp |
| | 65 | | | | | 70 | | | | | | 75 | | | | 80 |
| 5 | Tyr | Val | Asn | Thr | Ile | Pro | Thr | Ser | Met | Glu | Pro | Asp | Phe | Pro | Gly | Asp |
| | | | | | 85 | | | | | 90 | | | | | | 95 |
| | Glu | Glu | Met | Glu | Lys | Arg | Tyr | Arg | Arg | Trp | Met | Arg | Trp | Asn | Ala | Ala |
| | | | | 100 | | | | | 105 | | | | | 110 | | |
| 10 | Ile | Met | Val | His | Arg | Ala | Gln | Arg | Pro | Gly | Ile | Gly | Val | Gly | Gly | His |
| | | | 115 | | | | | 120 | | | | | 125 | | | |
| | Ile | Ser | Thr | Tyr | Ala | Gly | Ala | Ala | Pro | Leu | Tyr | Glu | Val | Gly | Phe | Asn |
| | | 130 | | | | | 135 | | | | | 140 | | | | |
| 15 | His | Phe | Phe | Arg | Gly | Lys | Asp | His | Pro | Gly | Gly | Gly | Asp | Gln | Val | Phe |
| | 145 | | | | | 150 | | | | 155 | | | | | | 160 |
| | Phe | Gln | Gly | His | Ala | Ser | Pro | Gly | Met | Tyr | Ala | Arg | Ala | Phe | Leu | Glu |
| | | | | 165 | | | | | | 170 | | | | | | 175 |
| 20 | Gly | Arg | Leu | Thr | Glu | Ser | Asp | Leu | Asp | Ser | Phe | Arg | Gln | Glu | Val | Ser |
| | | | | 180 | | | | | 185 | | | | | 190 | | |
| | Tyr | Glu | Gly | Gly | Gly | Ile | Pro | Ser | Tyr | Pro | His | Pro | His | Gly | Met | Pro |
| | | 195 | | | | | 200 | | | | | | 205 | | | |
| 25 | Asp | Phe | Trp | Glu | Phe | Pro | Thr | Val | Ser | Met | Gly | Leu | Gly | Pro | Met | Asp |
| | 210 | | | | | | 215 | | | | | 220 | | | | |
| | Ala | Ile | Tyr | Gln | Ala | Arg | Phe | Asn | Arg | Tyr | Leu | His | Asn | Arg | Gly | Ile |
| | 225 | | | | | 230 | | | | | 235 | | | | | 240 |
| 30 | Lys | Asp | Thr | Ser | Glu | Gln | His | Val | Trp | Ala | Phe | Leu | Gly | Asp | Gly | Glu |
| | | | | 245 | | | | | 250 | | | | | 255 | | |
| | Met | Asp | Glu | Pro | Glu | Ser | Arg | Gly | Leu | Ile | His | Gln | Ala | Ala | Leu | Asn |
| | | 260 | | | | | | 265 | | | | | | 270 | | |
| 35 | Asn | Leu | Asp | Asn | Leu | Thr | Phe | Val | Ile | Asn | Cys | Asn | Leu | Gln | Arg | Leu |
| | | 275 | | | | | | 280 | | | | | 285 | | | |
| | Asp | Gly | Pro | Val | Arg | Gly | Asn | Thr | Lys | Ile | Ile | Gln | Glu | Leu | Glu | Ser |
| | 290 | | | | | | 295 | | | | | 300 | | | | |
| 40 | Phe | Phe | Arg | Gly | Ala | Gly | Trp | Ser | Val | Ile | Lys | Val | Ile | Trp | Gly | Arg |
| | 305 | | | | | 310 | | | | | 315 | | | | | 320 |
| | Glu | Trp | Asp | Glu | Leu | Glu | Lys | Asp | Gln | Asp | Gly | Ala | Leu | Val | Glu | |
| | | | | 325 | | | | | 330 | | | | | 335 | | |
| 45 | Val | Met | Asn | Asn | Thr | Ser | Asp | Gly | Asp | Tyr | Gln | Thr | Phe | Lys | Ala | Asn |
| | | | | 340 | | | | | 345 | | | | | 350 | | |
| | Asp | Gly | Ala | Tyr | Val | Arg | Glu | His | Phe | Phe | Gly | Arg | Asp | Pro | Arg | Thr |
| | | 355 | | | | | | 360 | | | | 365 | | | | |
| 50 | Leu | Lys | Leu | Val | Glu | Asp | Met | Thr | Asp | Glu | Glu | Ile | Trp | Lys | Leu | Pro |
| | 370 | | | | | | 375 | | | | | 380 | | | | |
| | Arg | Gly | Gly | His | Asp | Tyr | Arg | Lys | Val | Tyr | Ala | Tyr | Lys | Arg | Ala | |
| 55 | 385 | | | | | | 390 | | | | 395 | | | | 400 | |

Leu Glu Thr Lys Asp Arg Pro Thr Val Ile Leu Ala His Thr Ile Lys
 405 410 415
 5 Gly Tyr Gly Leu Gly His Asn Phe Glu Gly Arg Asn Ala Thr His Gln
 420 425 430
 Met Lys Lys Leu Thr Leu Asp Asp Leu Lys Leu Phe Arg Asp Lys Gln
 435 440 445
 10 Gly Leu Pro Ile Thr Asp Glu Glu Leu Glu Lys Asp Pro Tyr Leu Pro
 450 455 460
 Pro Tyr Tyr His Pro Gly Glu Asp Ala Pro Glu Ile Lys Tyr Met Lys
 465 470 475 480
 15 Glu Arg Arg Gln Ala Leu Gly Gly Phe Leu Pro Glu Arg Arg Glu Lys
 485 490 495
 Tyr Glu Pro Leu Gln Val Pro Pro Leu Asp Lys Leu Arg Ser Val Arg
 500 505 510
 20 Lys Gly Ser Gly Lys Gln Gln Val Ala Thr Thr Met Ala Thr Val Arg
 515 520 525
 Thr Phe Lys Glu Leu Met Arg Asp Lys Asn Leu Ala Asp Arg Leu Val
 530 535 540
 25 Pro Ile Ile Pro Asp Glu Ala Arg Thr Phe Gly Leu Asp Ser Trp Phe
 545 550 555 560
 Pro Thr Leu Lys Ile Tyr Asn Pro His Gly Gln Asn Tyr Val Pro Val
 565 570 575
 30 Asp His Asp Leu Met Leu Ser Tyr Arg Glu Ala Lys Asp Gly Gln Ile
 580 585 590
 Leu His Glu Gly Ile Asn Glu Ala Gly Ser Val Ala Ser Phe Ile Ala
 595 600 605
 35 Ala Gly Thr Ser Tyr Ala Thr His Gly Glu Ala Met Ile Pro Leu Tyr
 610 615 620
 Ile Phe Tyr Ser Met Phe Gly Phe Gln Arg Thr Gly Asp Gly Ile Trp
 625 630 635 640
 40 Ala Ala Ala Asp Gln Met Thr Arg Gly Phe Leu Leu Gly Ala Thr Ala
 645 650 655
 Gly Arg Thr Thr Leu Thr Gly Glu Gly Leu Gln His Met Asp Gly His
 660 665 670
 45 Ser Pro Ile Leu Ala Ser Thr Asn Pro Gly Val Glu Thr Tyr Asp Pro
 675 680 685
 Ala Phe Ser Tyr Glu Ile Ala His Leu Val His Arg Gly Ile Asp Arg
 690 695 700
 50 Met Tyr Gly Pro Gly Lys Gly Glu Asn Val Ile Tyr Tyr Leu Thr Ile
 705 710 715 720
 Tyr Asn Glu Pro Thr Pro Gln Pro Ala Glu Pro Glu Asp Leu Asp Val
 725 730 735
 55 Glu Gly Leu His Lys Gly Ile Tyr Leu Tyr Asp Lys Ala Ala Glu Gly

740 745 750
 Glu Gly His Glu Ala Ser Ile Leu Ala Ser Gly Ile Gly Met Gln Trp
 5 755 760 765
 Ala Leu Arg Ala Arg Asp Ile Leu Ala Glu Asp Tyr Gly Ile Arg Ala
 770 775 780
 Asn Ile Phe Ser Ala Thr Ser Trp Val Glu Leu Ala Arg Asp Gly Ala
 785 790 795 800
 10 Arg Arg Asn Leu Glu Ala Leu Arg Asn Pro Gly Ala Asp Val Gly Glu
 805 810 815
 Ala Phe Val Thr Thr Gln Leu Lys Lys Gly Ser Gly Pro Tyr Val Ala
 820 825 830
 15 Val Ser Asp Phe Ala Thr Asp Leu Pro Asn Gln Ile Arg Glu Trp Val
 835 840 845
 Pro Gly Asp Tyr Ile Val Leu Gly Ala Asp Gly Phe Gly Phe Ser Asp
 850 855 860
 20 Thr Arg Pro Ala Ala Arg Arg Tyr Phe Asn Ile Asp Ala Glu Ser Ile
 865 870 875 880
 Val Val Ala Val Leu Arg Gly Leu Val Arg Glu Gly Val Ile Asp Ala
 885 890 895
 25 Ser Val Ala Ala His Ala Ala Glu Lys Tyr Lys Leu Ser Asp Pro Thr
 900 905 910
 Ala Pro Gln Val Asp Pro Asp Ala Pro Ile Glu
 915 920
 30
 <210> 23
 <211> 4013
 35 <212> DNA
 <213> Corynebacterium thermoaminogenes
 <220>
 40 <221> CDS
 <222> (319)..(3735)
 <400> 23
 45 gtccttttllg caaatlclgc aaagtgggla gaggicagat gtcagcaggt cggiccgatt 60
 lclglaggaa agtggagccg ttgggggcaa callaacctt ccccttggga tgtagclaaa 120
 cggcaatggg ggclcgggc ggggggcall ctlttccagg caaggltggg aaatlccgca 180
 ggicaciccc cggccggcgg tagagaacgg agcgaaaacg gaaagcaata cgiggttttc 240
 50 cggactggcc gttacgaigt lclgaagagt gacigccatc acccaacagg ctggicclcg 300
 tcgaaaggaa caaaaact gtg gtt aca aca aca ccc tcc acg ctg ccg gcg 351
 Val Val Thr Thr Thr Pro Ser Thr Leu Pro Ala
 1 5 10
 55 ttc aaa aag atc ctg gtg gcc aac cga ggt gaa atc gcg gtg cga gca 399

| | | | | | | | | | | | | | | | | | |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| | Phe | Lys | Lys | Ile | Leu | Val | Ala | Asn | Arg | Gly | Glu | Ile | Ala | Val | Arg | Ala | |
| | | | | 15 | | | | | 20 | | | | 25 | | | | |
| 5 | ttc | cgc | gcc | gcc | tac | gag | acc | ggg | gcc | gca | acc | gtg | gcc | atc | tac | ccc | 447 |
| | Phe | Arg | Ala | Ala | Tyr | Glu | Thr | Gly | Ala | Ala | Thr | Val | Ala | Ile | Tyr | Pro | |
| | | | | 30 | | | | | 35 | | | | 40 | | | | |
| | cgg | gag | gac | cgt | ggc | tcc | ttc | cac | cgc | tcc | ttc | gcc | tcc | gag | gcg | gtg | 495 |
| 10 | Arg | Glu | Asp | Arg | Gly | Ser | Phe | His | Arg | Ser | Phe | Ala | Ser | Glu | Ala | Val | |
| | | | | 45 | | | | 50 | | | | 55 | | | | | |
| | agg | alc | gga | acc | gag | ggc | tca | ccc | gtc | aag | gcg | tac | ctc | gat | att | gat | 543 |
| | Arg | Ile | Gly | Thr | Glu | Gly | Ser | Pro | Val | Lys | Ala | Tyr | Leu | Asp | Ile | Asp | |
| 15 | | | | 60 | | | | 65 | | | | 70 | | | | 75 | |
| | gag | alc | alc | aac | gcc | gcc | aag | aag | gtg | aaa | gcg | gac | gcg | gtc | tac | ccg | 591 |
| | Glu | Ile | Ile | Asn | Ala | Ala | Lys | Lys | Val | Lys | Ala | Asp | Ala | Val | Tyr | Pro | |
| | | | | 80 | | | | | 85 | | | | 90 | | | | |
| 20 | ggg | tat | ggt | ttc | ctt | tcg | gaa | aat | gcc | cag | ctc | gcg | cgt | gaa | tgc | gcg | 639 |
| | Gly | Tyr | Gly | Phe | Leu | Ser | Glu | Asn | Ala | Gln | Leu | Ala | Arg | Glu | Cys | Ala | |
| | | | | 95 | | | | | 100 | | | | 105 | | | | |
| | gag | aac | ggc | att | acc | ttc | atc | ggt | ccc | acc | ccg | gag | gtg | ctc | gac | ctc | 687 |
| 25 | Glu | Asn | Gly | Ile | Thr | Phe | Ile | Gly | Pro | Thr | Pro | Glu | Val | Leu | Asp | Leu | |
| | | | | 110 | | | | 115 | | | | 120 | | | | | |
| | acg | ggc | gac | aag | tcc | aag | gct | gtg | tcc | gcc | gcg | aag | aag | gcc | ggg | ctg | 735 |
| | Thr | Gly | Asp | Lys | Ser | Lys | Ala | Val | Ser | Ala | Ala | Lys | Lys | Ala | Gly | Leu | |
| 30 | | | | 125 | | | | 130 | | | | 135 | | | | | |
| | ccg | gtg | ctg | gcg | gaa | tcc | acc | ccc | agc | acc | gac | atc | gat | gag | atc | gtc | 783 |
| | Pro | Val | Leu | Ala | Glu | Ser | Thr | Pro | Ser | Thr | Asp | Ile | Asp | Glu | Ile | Val | |
| | | | | 140 | | | | 145 | | | | 150 | | | | 155 | |
| 35 | aag | agt | gcc | gag | ggg | cag | acc | tac | ccg | atc | ttc | gtc | aag | gcc | gtc | gca | 831 |
| | Lys | Ser | Ala | Glu | Gly | Gln | Thr | Tyr | Pro | Ile | Phe | Val | Lys | Ala | Val | Ala | |
| | | | | 160 | | | | | 165 | | | 170 | | | | | |
| | ggt | ggt | ggc | ggg | cgt | ggt | atg | cgg | ttc | gtc | gag | aag | ccc | gag | gac | ctg | 879 |
| 40 | Gly | Gly | Gly | Gly | Arg | Gly | Met | Arg | Phe | Val | Glu | Lys | Pro | Glu | Asp | Leu | |
| | | | | 175 | | | | | 180 | | | | 185 | | | | |
| | cgt | gag | ctg | gcc | agg | gag | gcc | tcc | cgc | gag | gcg | gag | gcc | gct | ttc | ggt | 927 |
| | Arg | Glu | Leu | Ala | Arg | Glu | Ala | Ser | Arg | Glu | Ala | Glu | Ala | Ala | Phe | Gly | |
| 45 | | | | 190 | | | | 195 | | | | 200 | | | | | |
| | gac | gga | tcc | gtc | tac | gtc | gaa | cgg | gcc | gtg | alc | aaa | ccc | cag | cac | atc | 975 |
| | Asp | Gly | Ser | Val | Tyr | Val | Glu | Arg | Ala | Val | Ile | Lys | Pro | Gln | His | Ile | |
| | | | | 205 | | | | 210 | | | | 215 | | | | | |
| 50 | gag | gtg | cag | atc | ctc | ggt | gat | cac | acc | ggc | gat | gtc | atc | cac | ctg | tat | 1023 |
| | Glu | Val | Gln | Ile | Leu | Gly | Asp | His | Thr | Gly | Asp | Val | Ile | His | Leu | Tyr | |
| | | | | 220 | | | | 225 | | | | 230 | | | | 235 | |
| | gaa | cgc | gac | tgt | tcc | ctg | cag | cgc | cgc | cac | cag | aag | gtc | gtg | gag | atc | 1071 |
| 55 | Glu | Arg | Asp | Cys | Ser | Leu | Gln | Arg | Arg | His | Gln | Lys | Val | Val | Glu | Ile | |

| | | | | |
|----|---|------|-----|-----|
| | 240 | 245 | 250 | |
| | gca cct gcc cag cac ctc gac ccg gag ctg cgc gac cgc atc tgt gcc | 1119 | | |
| 5 | Ala Pro Ala Gln His Leu Asp Pro Glu Leu Arg Asp Arg Ile Cys Ala | | | |
| | 255 | 260 | 265 | |
| | gag gcc gtg aag ttc tgc aaa tcc atc gga tac cag ggc gcc ggc acc | 1167 | | |
| | Asp Ala Val Lys Phe Cys Lys Ser Ile Gly Tyr Gln Gly Ala Gly Thr | | | |
| 10 | 270 | 275 | 280 | |
| | gtg gag ttc ctc gtc gac gag gcg ggc aac cac gtc ttc att gag atg | 1215 | | |
| | Val Glu Phe Leu Val Asp Glu Ala Gly Asn His Val Phe Ile Glu Met | | | |
| | 285 | 290 | 295 | |
| 15 | aac ccc cgc atc cag gtg gaa cac acc gtg acc gag gag gtc acc tcc | 1263 | | |
| | Asn Pro Arg Ile Gln Val Glu His Thr Val Thr Glu Glu Val Thr Ser | | | |
| | 300 | 305 | 310 | 315 |
| | gtc gac ctg gtc aag gcg cag atg cac ctg gcc gcc ggt gcc acc ctg | 1311 | | |
| 20 | Val Asp Leu Val Lys Ala Gln Met His Leu Ala Ala Gly Ala Thr Leu | | | |
| | 320 | 325 | 330 | |
| | aag gaa ctg ggc ctg acc cag gac aag atc acc acc cac ggt gcc gcc | 1359 | | |
| | Lys Glu Leu Gly Leu Thr Gln Asp Lys Ile Thr Thr His Gly Ala Ala | | | |
| 25 | 335 | 340 | 345 | |
| | ctg cag tgc cgc atc acc acg gag gac ccg tcc aac aac ttc cgg ccc | 1407 | | |
| | Leu Gln Cys Arg Ile Thr Thr Glu Asp Pro Ser Asn Asn Phe Arg Pro | | | |
| | 350 | 355 | 360 | |
| 30 | gac acc ggt gtg atc acc gcc tac cgc tcc ccg ggt ggt gcg ggt gtg | 1455 | | |
| | Asp Thr Gly Val Ile Thr Ala Tyr Arg Ser Pro Gly Gly Ala Gly Val | | | |
| | 365 | 370 | 375 | |
| | cgt ctc gac ggc gca gcc cag ctc ggc ggc gag atc acc gca cat ttc | 1503 | | |
| 35 | Arg Leu Asp Gly Ala Ala Gln Leu Gly Gly Glu Ile Thr Ala His Phe | | | |
| | 380 | 385 | 390 | 395 |
| | gag tcc atg ctg gtc aag atg acc tgc cgc ggt tcc gat ttc gag acc | 1551 | | |
| | Asp Ser Met Leu Val Lys Met Thr Cys Arg Gly Ser Asp Phe Glu Thr | | | |
| 40 | 400 | 405 | 410 | |
| | gcc gtg tcc cga gcc cag cgc gcc ctg gcg gag ttc aac gtc tcc ggc | 1599 | | |
| | Ala Val Ser Arg Ala Gln Arg Ala Leu Ala Glu Phe Asn Val Ser Gly | | | |
| | 415 | 420 | 425 | |
| 45 | gtg gcc acc aac atc ggc ttc ctg cgt gcg ctg ctg cgc gag gaa gac | 1647 | | |
| | Val Ala Thr Asn Ile Gly Phe Leu Arg Ala Leu Leu Arg Glu Glu Asp | | | |
| | 430 | 435 | 440 | |
| | ttc acc aag agg cgc atc gac acc ggc ttc atc ggc tcc cac cag cac | 1695 | | |
| 50 | Phe Thr Lys Arg Arg Ile Asp Thr Gly Phe Ile Gly Ser His Gln His | | | |
| | 445 | 450 | 455 | |
| | ctg ctc cag gcc cca ccg gcc gac gat gag cag ggg cgg atc ctg gaa | 1743 | | |
| 55 | Leu Leu Gln Ala Pro Pro Ala Asp Asp Glu Gln Gly Arg Ile Leu Glu | | | |
| | 460 | 465 | 470 | 475 |

| | | |
|----|---|------|
| | tac ctg gcg gat gtc acc gtg aac aaa ccc cac ggt gaa cgc ccc gag | 1791 |
| | Tyr Leu Ala Asp Val Thr Val Asn Lys Pro His Gly Glu Arg Pro Glu | |
| 5 | 480 485 490 | |
| | aca gcc cgt ccg ata gag aag ctg ccc gag gtg gag aac atc ccg ctg | 1839 |
| | Thr Ala Arg Pro Ile Glu Lys Leu Pro Glu Val Glu Asn Ile Pro Leu | |
| | 495 500 505 | |
| 10 | cca cgc ggc tcc cgc gac cgc ctg aag cag ctc ggc ccg gag ggt ttc | 1887 |
| | Pro Arg Gly Ser Arg Asp Arg Leu Lys Gln Leu Gly Pro Glu Gly Phe | |
| | 510 515 520 | |
| | gcc cgc gat ctg cgc gaa cag gat gcc ctg gcc gtc acc gac acc acc | 1935 |
| 15 | Ala Arg Asp Leu Arg Glu Gln Asp Ala Leu Ala Val Thr Asp Thr Thr | |
| | 525 530 535 | |
| | ttc cgc gat gcc cac cag tcc ctc ctg gcc acc cgc gtg cgc tcc ttc | 1983 |
| | Phe Arg Asp Ala His Gln Ser Leu Leu Ala Thr Arg Val Arg Ser Phe | |
| 20 | 540 545 550 555 | |
| | gcg ctg acc ccg gcg gcg cgc gcc gtc gca aag ctc acc ccc gag ctg | 2031 |
| | Ala Leu Thr Pro Ala Ala Arg Ala Val Ala Lys Leu Thr Pro Glu Leu | |
| | 560 565 570 | |
| 25 | ctg tcg gtg gag gcc tgg ggc ggt gcc acc tac gac gtg gcc atg cgc | 2079 |
| | Leu Ser Val Glu Ala Trp Gly Gly Ala Thr Tyr Asp Val Ala Met Arg | |
| | 575 580 585 | |
| | ttc ctc ttc gag gat ccg tgg gca cgc ctg gat gag ctg cgt gag gcg | 2127 |
| 30 | Phe Leu Phe Glu Asp Pro Trp Ala Arg Leu Asp Glu Leu Arg Glu Ala | |
| | 590 595 600 | |
| | atg ccg aat gtg aac atc cag atg ctg ctg cgt ggt cgc aac acc gtc | 2175 |
| | Met Pro Asn Val Asn Ile Gln Met Leu Leu Arg Gly Arg Asn Thr Val | |
| 35 | 605 610 615 | |
| | ggg tac acc ccg tac ccc gat tcg gtg tgc cgc gcg ttt gtg cag gag | 2223 |
| | Gly Tyr Thr Pro Tyr Pro Asp Ser Val Cys Arg Ala Phe Val Gln Glu | |
| | 620 625 630 635 | |
| 40 | gcc gcc aag tcc ggt gtg gac atc ttc cgc atc ttc gac gcg ctc aac | 2271 |
| | Ala Ala Lys Ser Gly Val Asp Ile Phe Arg Ile Phe Asp Ala Leu Asn | |
| | 640 645 650 | |
| | gac atc tcc cag atg cgc ccg gcc atc gac gcc gtc ctg gag acc ggc | 2319 |
| 45 | Asp Ile Ser Gln Met Arg Pro Ala Ile Asp Ala Val Leu Glu Thr Gly | |
| | 655 660 665 | |
| | acc agt gtt gcc gag gtc gcc atg gcg tac tcc ggt gac ctg tcc aat | 2367 |
| | Thr Ser Val Ala Glu Val Ala Met Ala Tyr Ser Gly Asp Leu Ser Asn | |
| 50 | 670 675 680 | |
| | ccg ggg gag aag ctc tac acc ctg gac tac tac ctg aac ctg gcc gag | 2415 |
| | Pro Gly Glu Lys Leu Tyr Thr Leu Asp Tyr Tyr Leu Asn Leu Ala Glu | |
| | 685 690 695 | |
| 55 | cag atc gtc gac tcc ggt gca cac atc ctg gcc atc aag gac atg gcc | 2463 |

| | | | | | | | | | | | | | | | | | |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| | Gln | Ile | Val | Asp | Ser | Gly | Ala | His | Ile | Leu | Ala | Ile | Lys | Asp | Met | Ala | |
| | 700 | | | | | 705 | | | | 710 | | | | | 715 | | |
| 5 | ggc | ctg | ctg | cgc | cgc | gcc | gcg | gcg | ccc | aaa | ctg | gtc | acc | gcc | ctg | cgc | 2511 |
| | Gly | Leu | Leu | Arg | Arg | Ala | Ala | Ala | Pro | Lys | Leu | Val | Thr | Ala | Leu | Arg | |
| | | | | | 720 | | | | | 725 | | | | | 730 | | |
| 10 | cgt | gaa | ttc | gac | ctg | ccc | gtg | cat | gtc | cac | acc | cac | gac | acc | gcc | ggc | 2559 |
| | Arg | Glu | Phe | Asp | Leu | Pro | Val | His | Val | His | Thr | His | Asp | Thr | Ala | Gly | |
| | | | | 735 | | | | | 740 | | | | 745 | | | | |
| | ggt | cag | ctg | gcc | acc | tac | ctg | gcc | gcc | gcc | aac | gcc | ggg | gcc | gat | gcc | 2607 |
| | Gly | Gln | Leu | Ala | Thr | Tyr | Leu | Ala | Ala | Ala | Asn | Ala | Gly | Ala | Asp | Ala | |
| 15 | | | 750 | | | | | 755 | | | | 760 | | | | | |
| | gtc | gac | gcc | gcc | tcc | gca | ccc | ctg | tcc | ggt | acc | acc | tcc | cag | ccg | tcc | 2655 |
| | Val | Asp | Ala | Ala | Ser | Ala | Pro | Leu | Ser | Gly | Thr | Thr | Ser | Gln | Pro | Ser | |
| | | | 765 | | | 770 | | | | | 775 | | | | | | |
| 20 | atg | tcc | gct | ctg | gtt | gcc | gcg | ttt | gcg | cac | acc | cga | cgc | gac | acc | ggc | 2703 |
| | Met | Ser | Ala | Leu | Val | Ala | Ala | Phe | Ala | His | Thr | Arg | Arg | Asp | Thr | Gly | |
| | 780 | | | | | 785 | | | | 790 | | | | 795 | | | |
| 25 | ctc | aac | ctg | cag | gcc | gtc | tcc | gac | ctg | gaa | ccg | tac | tgg | gag | gcg | gtc | 2751 |
| | Leu | Asn | Leu | Gln | Ala | Val | Ser | Asp | Leu | Glu | Pro | Tyr | Trp | Glu | Ala | Val | |
| | | | | 800 | | | | 805 | | | | 810 | | | | | |
| | cgc | gga | ctg | tac | ctg | ccg | ttt | gaa | tcc | ggc | acc | ccg | ggc | ccg | acc | gga | 2799 |
| | Arg | Gly | Leu | Tyr | Leu | Pro | Phe | Glu | Ser | Gly | Thr | Pro | Gly | Pro | Thr | Gly | |
| 30 | | | 815 | | | | | 820 | | | | 825 | | | | | |
| | cgc | gtt | tac | cgc | cac | gag | atc | ccc | ggc | ggt | cag | ctg | tcc | aac | ctg | cgt | 2847 |
| | Arg | Val | Tyr | Arg | His | Glu | Ile | Pro | Gly | Gly | Gln | Leu | Ser | Asn | Leu | Arg | |
| | | | 830 | | | | | 835 | | | | 840 | | | | | |
| 35 | gcc | cag | gcc | gtt | gca | ctg | ggt | ctg | gcc | gac | cgc | ttc | gag | ctc | atc | gag | 2895 |
| | Ala | Gln | Ala | Val | Ala | Leu | Gly | Leu | Ala | Asp | Arg | Phe | Glu | Leu | Ile | Glu | |
| | | | 845 | | | 850 | | | | | 855 | | | | | | |
| 40 | gac | tac | tac | gcg | gcc | gtc | aac | gag | atg | ctg | ggt | cgt | ccg | acc | aag | gtc | 2943 |
| | Asp | Tyr | Tyr | Ala | Ala | Val | Asn | Glu | Met | Leu | Gly | Arg | Pro | Thr | Lys | Val | |
| | 860 | | | | | 865 | | | | 870 | | | | 875 | | | |
| | acc | ccg | tcc | tcc | aag | gtt | gtc | ggt | gac | ctc | gca | ctg | cac | ctc | gtc | ggt | 2991 |
| | Thr | Pro | Ser | Ser | Lys | Val | Val | Gly | Asp | Leu | Ala | Leu | His | Leu | Val | Gly | |
| 45 | | | | | 880 | | | | | 885 | | | | 890 | | | |
| | gcc | ggt | gtg | agc | ccg | gag | gat | ttc | gcc | gcc | gat | ccg | cag | aag | tac | gac | 3039 |
| | Ala | Gly | Val | Ser | Pro | Glu | Asp | Phe | Ala | Ala | Asp | Pro | Gln | Lys | Tyr | Asp | |
| | | | | 895 | | | | 900 | | | | 905 | | | | | |
| 50 | atc | ccc | gat | tcc | gtc | atc | gcc | ttc | ctc | cgc | ggc | gaa | ctg | ggt | acc | ccg | 3087 |
| | Ile | Pro | Asp | Ser | Val | Ile | Ala | Phe | Leu | Arg | Gly | Glu | Leu | Gly | Thr | Pro | |
| | | | | 910 | | | | 915 | | | | 920 | | | | | |
| 55 | ccc | ggt | ggc | tgg | ccc | gaa | ccg | ctg | cgc | acc | cgt | gca | ctc | gag | ggt | cgc | 3135 |
| | Pro | Gly | Gly | Trp | Pro | Glu | Pro | Leu | Arg | Thr | Arg | Ala | Leu | Glu | Gly | Arg | |

925 930 935
 1cc cag ggt aag gcc ccg ctg gcg gag atc ccc gcc gag gag cag gcc 3183
 Ser Gln Gly Lys Ala Pro Leu Ala Glu Ile Pro Ala Glu Glu Gln Ala
 940 945 950 955
 cac ctg gat tcc gat gat tcc gcg gag cgt cgc ggc acc ctg aac cgc 3231
 His Leu Asp Ser Asp Asp Ser Ala Glu Arg Arg Gly Thr Leu Asn Arg
 960 965 970
 ctg ctg ttc ccg aag ccg acc gag gag ttc ctt gag cac cgt cgc cgc 3279
 Leu Leu Phe Pro Lys Pro Thr Glu Glu Phe Leu Glu His Arg Arg Arg
 975 980 985
 ttc ggc aac acc tcc gcc ctg gat gac cgc gag ttc ttc tac ggc ttg 3327
 Phe Gly Asn Thr Ser Ala Leu Asp Asp Arg Glu Phe Phe Tyr Gly Leu
 990 995 1000
 aag gag gga cgt gag gag ctg atc cga ctg acc ggt gtg tcc acc ccg 3375
 Lys Glu Gly Arg Glu Glu Leu Ile Arg Leu Thr Gly Val Ser Thr Pro
 1005 1010 1015
 alg gtg gtc cgc ctg gat gcg gtg tcc gaa ccg gat gac aaa ggc atg 3423
 Met Val Val Arg Leu Asp Ala Val Ser Glu Pro Asp Asp Lys Gly Met
 1020 1025 1030 1035
 cgc aac glg gtg gtc aac gtc aac ggc cag atc cgc ccg atc aag gtg 3471
 Arg Asn Val Val Val Asn Val Asn Gly Gln Ile Arg Pro Ile Lys Val
 1040 1045 1050
 cgc gac cgt tcc glg gag tcc gtc acc gcc acc gcg gag aag gcc gat 3519
 Arg Asp Arg Ser Val Glu Ser Val Thr Ala Thr Ala Glu Lys Ala Asp
 1055 1060 1065
 gcc acc aac aag ggc cal gtc gcc gca cca ttc gcc ggt gtg gtc acc 3567
 Ala Thr Asn Lys Gly His Val Ala Ala Pro Phe Ala Gly Val Val Thr
 1070 1075 1080
 gtg acc gtc gcc gag ggt gat gag atc aag gct ggc gac gcc gtg gcc 3615
 Val Thr Val Ala Glu Gly Asp Glu Ile Lys Ala Gly Asp Ala Val Ala
 1085 1090 1095
 atc att gag gcc alg aag alg gag gcc acc atc acc gcg cct gtc gac 3663
 Ile Ile Glu Ala Met Lys Met Glu Ala Thr Ile Thr Ala Pro Val Asp
 1100 1105 1110 1115
 ggt gtc atc gac cgc gtc gtg gtg ccc gcc gcc acc aag gtc gag ggc 3711
 Gly Val Ile Asp Arg Val Val Val Pro Ala Ala Thr Lys Val Glu Gly
 1120 1125 1130
 ggc gac ctg atc gtg gtc glg tcc tagcgaciga gagccacaac ccgtcccg 3765
 Gly Asp Leu Ile Val Val Val Ser
 1135
 igcctiglit tcaacctccc ccgatgaig tttcagggg gaggtcttac giacctcacc 3825
 glgacggigc algatatacg tctgtctgga gagaatgctc caggtaggaa cgccaaccac 3885
 cccactccgt gatgtccgt gctgatccca ggcaggccgg ttggaaagaa aaaccagiga 3945

lggaacggcc atcggacagc gagacggaac caagcgical cggctccggt agagcggiga 4005
 ggagcccg 4013

5 <210> 24
 <211> 1139
 <212> PRT
 10 <213> Corynebacterium thermoaminogenes
 <400> 24
 Val Val Thr Thr Thr Pro Ser Thr Leu Pro Ala Phe Lys Lys Ile Leu
 1 5 10 15
 Val Ala Asn Arg Gly Glu Ile Ala Val Arg Ala Phe Arg Ala Ala Tyr
 15 20 25 30
 Glu Thr Gly Ala Ala Thr Val Ala Ile Tyr Pro Arg Glu Asp Arg Gly
 35 40 45
 Ser Phe His Arg Ser Phe Ala Ser Glu Ala Val Arg Ile Gly Thr Glu
 20 50 55 60
 Gly Ser Pro Val Lys Ala Tyr Leu Asp Ile Asp Glu Ile Ile Asn Ala
 65 70 75 80
 Ala Lys Lys Val Lys Ala Asp Ala Val Tyr Pro Gly Tyr Gly Phe Leu
 25 85 90 95
 Ser Glu Asn Ala Gln Leu Ala Arg Glu Cys Ala Glu Asn Gly Ile Thr
 100 105 110
 Phe Ile Gly Pro Thr Pro Glu Val Leu Asp Leu Thr Gly Asp Lys Ser
 30 115 120 125
 Lys Ala Val Ser Ala Ala Lys Lys Ala Gly Leu Pro Val Leu Ala Glu
 130 135 140
 Ser Thr Pro Ser Thr Asp Ile Asp Glu Ile Val Lys Ser Ala Glu Gly
 35 145 150 155 160
 Gln Thr Tyr Pro Ile Phe Val Lys Ala Val Ala Gly Gly Gly Gly Arg
 165 170 175
 Gly Met Arg Phe Val Glu Lys Pro Glu Asp Leu Arg Glu Leu Ala Arg
 40 180 185 190
 Glu Ala Ser Arg Glu Ala Glu Ala Ala Phe Gly Asp Gly Ser Val Tyr
 195 200 205
 Val Glu Arg Ala Val Ile Lys Pro Gln His Ile Glu Val Gln Ile Leu
 45 210 215 220
 Gly Asp His Thr Gly Asp Val Ile His Leu Tyr Glu Arg Asp Cys Ser
 225 230 235 240
 Leu Gln Arg Arg His Gln Lys Val Val Glu Ile Ala Pro Ala Gln His
 50 245 250 255
 Leu Asp Pro Glu Leu Arg Asp Arg Ile Cys Ala Asp Ala Val Lys Phe
 260 265 270
 55 Cys Lys Ser Ile Gly Tyr Gln Gly Ala Gly Thr Val Glu Phe Leu Val

275 280 285
 Asp Glu Ala Gly Asn His Val Phe Ile Glu Met Asn Pro Arg Ile Gln
 290 295 300
 5 Val Glu His Thr Val Thr Glu Glu Val Thr Ser Val Asp Leu Val Lys
 305 310 315 320
 Ala Gln Met His Leu Ala Ala Gly Ala Thr Leu Lys Glu Leu Gly Leu
 10 325 330 335
 Thr Gln Asp Lys Ile Thr Thr His Gly Ala Ala Leu Gln Cys Arg Ile
 340 345 350
 Thr Thr Glu Asp Pro Ser Asn Asn Phe Arg Pro Asp Thr Gly Val Ile
 15 355 360 365
 Thr Ala Tyr Arg Ser Pro Gly Gly Ala Gly Val Arg Leu Asp Gly Ala
 370 375 380
 20 Ala Gln Leu Gly Gly Glu Ile Thr Ala His Phe Asp Ser Met Leu Val
 385 390 395 400
 Lys Met Thr Cys Arg Gly Ser Asp Phe Glu Thr Ala Val Ser Arg Ala
 405 410 415
 Gln Arg Ala Leu Ala Glu Phe Asn Val Ser Gly Val Ala Thr Asn Ile
 25 420 425 430
 Gly Phe Leu Arg Ala Leu Leu Arg Glu Glu Asp Phe Thr Lys Arg Arg
 435 440 445
 Ile Asp Thr Gly Phe Ile Gly Ser His Gln His Leu Leu Gln Ala Pro
 30 450 455 460
 Pro Ala Asp Asp Glu Gln Gly Arg Ile Leu Glu Tyr Leu Ala Asp Val
 465 470 475 480
 Thr Val Asn Lys Pro His Gly Glu Arg Pro Glu Thr Ala Arg Pro Ile
 35 485 490 495
 Glu Lys Leu Pro Glu Val Glu Asn Ile Pro Leu Pro Arg Gly Ser Arg
 500 505 510
 Asp Arg Leu Lys Gln Leu Gly Pro Glu Gly Phe Ala Arg Asp Leu Arg
 40 515 520 525
 Glu Gln Asp Ala Leu Ala Val Thr Asp Thr Thr Phe Arg Asp Ala His
 530 535 540
 Gln Ser Leu Leu Ala Thr Arg Val Arg Ser Phe Ala Leu Thr Pro Ala
 45 545 550 555 560
 Ala Arg Ala Val Ala Lys Leu Thr Pro Glu Leu Leu Ser Val Glu Ala
 565 570 575
 Trp Gly Gly Ala Thr Tyr Asp Val Ala Met Arg Phe Leu Phe Glu Asp
 50 580 585 590
 Pro Trp Ala Arg Leu Asp Glu Leu Arg Glu Ala Met Pro Asn Val Asn
 595 600 605
 55 Ile Gln Met Leu Leu Arg Gly Arg Asn Thr Val Gly Tyr Thr Pro Tyr
 610 615 620

Pro Asp Ser Val Cys Arg Ala Phe Val Gln Glu Ala Ala Lys Ser Gly
 625 630 635 640
 Val Asp Ile Phe Arg Ile Phe Asp Ala Leu Asn Asp Ile Ser Gln Met
 5 645 650 655
 Arg Pro Ala Ile Asp Ala Val Leu Glu Thr Gly Thr Ser Val Ala Glu
 660 665 670
 Val Ala Met Ala Tyr Ser Gly Asp Leu Ser Asn Pro Gly Glu Lys Leu
 10 675 680 685
 Tyr Thr Leu Asp Tyr Tyr Leu Asn Leu Ala Glu Gln Ile Val Asp Ser
 690 695 700
 Gly Ala His Ile Leu Ala Ile Lys Asp Met Ala Gly Leu Leu Arg Arg
 15 705 710 715 720
 Ala Ala Ala Pro Lys Leu Val Thr Ala Leu Arg Arg Glu Phe Asp Leu
 725 730 735
 Pro Val His Val His Thr His Asp Thr Ala Gly Gly Gln Leu Ala Thr
 20 740 745 750
 Tyr Leu Ala Ala Ala Asn Ala Gly Ala Asp Ala Val Asp Ala Ala Ser
 755 760 765
 Ala Pro Leu Ser Gly Thr Thr Ser Gln Pro Ser Met Ser Ala Leu Val
 25 770 775 780
 Ala Ala Phe Ala His Thr Arg Arg Asp Thr Gly Leu Asn Leu Gln Ala
 785 790 795 800
 Val Ser Asp Leu Glu Pro Tyr Trp Glu Ala Val Arg Gly Leu Tyr Leu
 30 805 810 815
 Pro Phe Glu Ser Gly Thr Pro Gly Pro Thr Gly Arg Val Tyr Arg His
 820 825 830
 Glu Ile Pro Gly Gly Gln Leu Ser Asn Leu Arg Ala Gln Ala Val Ala
 35 835 840 845
 Leu Gly Leu Ala Asp Arg Phe Glu Leu Ile Glu Asp Tyr Tyr Ala Ala
 850 855 860
 Val Asn Glu Met Leu Gly Arg Pro Thr Lys Val Thr Pro Ser Ser Lys
 40 865 870 875 880
 Val Val Gly Asp Leu Ala Leu His Leu Val Gly Ala Gly Val Ser Pro
 885 890 895
 Glu Asp Phe Ala Ala Asp Pro Gln Lys Tyr Asp Ile Pro Asp Ser Val
 45 900 905 910
 Ile Ala Phe Leu Arg Gly Glu Leu Gly Thr Pro Pro Gly Gly Trp Pro
 915 920 925
 Glu Pro Leu Arg Thr Arg Ala Leu Glu Gly Arg Ser Gln Gly Lys Ala
 50 930 935 940
 Pro Leu Ala Glu Ile Pro Ala Glu Glu Gln Ala His Leu Asp Ser Asp
 945 950 955 960
 Asp Ser Ala Glu Arg Arg Gly Thr Leu Asn Arg Leu Leu Phe Pro Lys
 55

965 970 975
 Pro Thr Glu Glu Phe Leu Glu His Arg Arg Arg Phe Gly Asn Thr Ser
 980 985 990
 5 Ala Leu Asp Asp Arg Glu Phe Phe Tyr Gly Leu Lys Glu Gly Arg Glu
 995 1000 1005
 Glu Leu Ile Arg Leu Thr Gly Val Ser Thr Pro Met Val Val Arg Leu
 1010 1015 1020
 10 Asp Ala Val Ser Glu Pro Asp Asp Lys Gly Met Arg Asn Val Val Val
 025 1030 1035 1040
 Asn Val Asn Gly Gln Ile Arg Pro Ile Lys Val Arg Asp Arg Ser Val
 15 1045 1050 1055
 Glu Ser Val Thr Ala Thr Ala Glu Lys Ala Asp Ala Thr Asn Lys Gly
 1060 1065 1070
 His Val Ala Ala Pro Phe Ala Gly Val Val Thr Val Thr Val Ala Glu
 20 1075 1080 1085
 Gly Asp Glu Ile Lys Ala Gly Asp Ala Val Ala Ile Ile Glu Ala Met
 1090 1095 1100
 Lys Met Glu Ala Thr Ile Thr Ala Pro Val Asp Gly Val Ile Asp Arg
 25 1105 1110 1115 1120
 Val Val Val Pro Ala Ala Thr Lys Val Glu Gly Gly Asp Leu Ile Val
 1125 1130 1135
 Val Val Ser
 30
 <210> 25
 <211> 3306
 35 <212> DNA
 <213> *Corynebacterium thermoaminogenes*
 <220>
 40 <221> CDS
 <222> (64)..(2820)
 <400> 25
 45 gatcaaccia agccaggaga atccggcggg cggtttctac ttctacagga gctgaacccc 60
 acc gtg aat gaa ctt ctc cgt gac gat atc cgt tat ctc ggc cgg atc 108
 Val Asn Glu Leu Leu Arg Asp Asp Ile Arg Tyr Leu Gly Arg Ile
 1 5 10 15
 50 ctg ggc gag gtg atc tcc gag cag gag ggc cac cat gtc ttc gaa ctg 156
 Leu Gly Glu Val Ile Ser Glu Gln Glu Gly His His Val Phe Glu Leu
 20 25 30
 55 gtt gaa cgc gcc cgc cgg acc tcc ttc gac atc gcc aag gga cgc gcg 204
 Val Glu Arg Ala Arg Arg Thr Ser Phe Asp Ile Ala Lys Gly Arg Ala

| | | | | |
|----|---|-----|-----|-----|
| | 35 | 40 | 45 | 252 |
| | gag atg gac agt ctg glg gag glg ttc gct ggc atc gac ccg gag gac | | | |
| | Glu Met Asp Ser Leu Val Glu Val Phe Ala Gly Ile Asp Pro Glu Asp | | | |
| 5 | 50 | 55 | 60 | |
| | gcc acg ccc glg gcc cga gcc ttc acc cat ttc gcc ctg ttg gcc aac | | | 300 |
| | Ala Thr Pro Val Ala Arg Ala Phe Thr His Phe Ala Leu Leu Ala Asn | | | |
| 10 | 65 | 70 | 75 | |
| | ctc gcg gag gat ttg cat gac gca gcc cag cgg gaa cag gcc ctg aac | | | 348 |
| | Leu Ala Glu Asp Leu His Asp Ala Ala Gln Arg Glu Gln Ala Leu Asn | | | |
| 15 | 80 | 85 | 90 | 95 |
| | tcg ggt gag ccc gcg ccg gac agc acc ctc gag gcc acc tgg gtg aaa | | | 396 |
| | Ser Gly Glu Pro Ala Pro Asp Ser Thr Leu Glu Ala Thr Trp Val Lys | | | |
| | 100 | 105 | 110 | |
| | ctg gat gat gcc ggg glg ggc agc ggt gag glc gcc gcg gtg atc cgc | | | 444 |
| | Leu Asp Asp Ala Gly Val Gly Ser Gly Glu Val Ala Ala Val Ile Arg | | | |
| 20 | 115 | 120 | 125 | |
| | aat gcg ctc glc gcc ccg glg ctc acc gcg cac ccg acg gaa acc cga | | | 492 |
| | Asn Ala Leu Val Ala Pro Val Leu Thr Ala His Pro Thr Glu Thr Arg | | | |
| 25 | 130 | 135 | 140 | |
| | cgt cgt acc glg ttc gac gcg cag aag cac atc acc gcc ctg atg gag | | | 540 |
| | Arg Arg Thr Val Phe Asp Ala Gln Lys His Ile Thr Ala Leu Met Glu | | | |
| | 145 | 150 | 155 | |
| | gaa cgc cac ctc ctc ctg gcg ctg ccc acc cat gcc cgg acc cag tcc | | | 588 |
| | Glu Arg His Leu Leu Leu Ala Leu Pro Thr His Ala Arg Thr Gln Ser | | | |
| 30 | 160 | 165 | 170 | 175 |
| | aag ctg gat gac atc gag cgc aac atc cgg cga cgg atc acg atc ctg | | | 636 |
| | Lys Leu Asp Asp Ile Glu Arg Asn Ile Arg Arg Arg Ile Thr Ile Leu | | | |
| 35 | 180 | 185 | 190 | |
| | tgg cag acg gcc ctc atc cgt gtg gcc cgt ccc cgc atc gag gat gag | | | 684 |
| | Trp Gln Thr Ala Leu Ile Arg Val Ala Arg Pro Arg Ile Glu Asp Glu | | | |
| 40 | 195 | 200 | 205 | |
| | glc gag gtt gga ctg cgc tac tac aag ctc agc ctg ttg gcc gag atc | | | 732 |
| | Val Glu Val Gly Leu Arg Tyr Tyr Lys Leu Ser Leu Leu Ala Glu Ile | | | |
| | 210 | 215 | 220 | |
| 45 | ccc cgc atc aat cat gat glg acc glg gaa ctg gcc cgg cgt ttc ggc | | | 780 |
| | Pro Arg Ile Asn His Asp Val Thr Val Glu Leu Ala Arg Arg Phe Gly | | | |
| | 225 | 230 | 235 | |
| | ggg gat atc ccc acc acg gcg atg gtc agg ccg gga tcc tgg atc ggc | | | 828 |
| | Gly Asp Ile Pro Thr Thr Ala Met Val Arg Pro Gly Ser Trp Ile Gly | | | |
| 50 | 240 | 245 | 250 | 255 |
| | ggg gac cat gat ggc aac ccc ttc gtc acc gcg gag act gtc acc tac | | | 876 |
| | Gly Asp His Asp Gly Asn Pro Phe Val Thr Ala Glu Thr Val Thr Tyr | | | |
| 55 | 260 | 265 | 270 | |

EP 1 219 712 A1

gcc acc cat cgg gcc gcg gag acc gtc ctc aag tac tac gtc aag caa 924
Ala Thr His Arg Ala Ala Glu Thr Val Leu Lys Tyr Tyr Val Lys Gln
275 280 285

5 ctc cac gcc ctc gaa cac gaa ctc agt ctc tcc gac cgg atg aac gtc 972
Leu His Ala Leu Glu His Glu Leu Ser Leu Ser Asp Arg Met Asn Val
290 295 300

10 atc agc gat gag ctc cgt gtc ctt gcc gat gcc gcc cag aat gac atg 1020
Ile Ser Asp Glu Leu Arg Val Leu Ala Asp Ala Gly Gln Asn Asp Met
305 310 315

15 ccc agc cgg gtt gat gaa ccc tac cgg cgg gcc atc cac gcc atg cgt 1068
Pro Ser Arg Val Asp Glu Pro Tyr Arg Arg Ala Ile His Gly Met Arg
320 325 330 335

ggc cgg atg ctc gcc acc acg gcc gcc ctc atc ggt gag gag gcc gtc 1116
Gly Arg Met Leu Ala Thr Thr Ala Ala Leu Ile Gly Glu Glu Ala Val
340 345 350

20 gag gcc acc tgg ttc aag acc ttc acg ccc tat acc gat acc cac gag 1164
Glu Gly Thr Trp Phe Lys Thr Phe Thr Pro Tyr Thr Asp Thr His Glu
355 360 365

25 ttc aaa cgc gac ctc gat atc gtc gat ggt tcc ctc aga atg tcc cgg 1212
Phe Lys Arg Asp Leu Asp Ile Val Asp Gly Ser Leu Arg Met Ser Arg
370 375 380

gac gac atc atc gcc gat gac cgt ctc gcc atg ctc cgc tgc gcc ctc 1260
Asp Asp Ile Ile Ala Asp Asp Arg Leu Ala Met Leu Arg Ser Ala Leu
385 390 395

30 gac agc ttc ggg ttc aac ctc tac tcc ctc gat ctc cgc cag aat tcc 1308
Asp Ser Phe Gly Phe Asn Leu Tyr Ser Leu Asp Leu Arg Gln Asn Ser
400 405 410 415

35 gac ggt ttc gag gat gtc ctc acc gaa ttc ttc gcc acc gcc cag acc 1356
Asp Gly Phe Glu Asp Val Leu Thr Glu Leu Phe Ala Thr Ala Gln Thr
420 425 430

40 gag aag aac tac cgc ggg ttc acg gag gcc gag aag ctc gac ctc ctc 1404
Glu Lys Asn Tyr Arg Gly Leu Thr Glu Ala Glu Lys Leu Asp Leu Leu
435 440 445

45 atc cgc gaa ctc agc aca ccc cgc cgc ctc atc cgc cac ggg gac ccg 1452
Ile Arg Glu Leu Ser Thr Pro Arg Pro Leu Ile Pro His Gly Asp Pro
450 455 460

gac tac tcc gag gcc acc aac cgt gaa ctc ggg att ttt tgc aag gcc 1500
Asp Tyr Ser Glu Ala Thr Asn Arg Glu Leu Gly Ile Phe Ser Lys Ala
465 470 475

50 gcg gag gcc gtc cgt aaa ttc ggt cct ctc atg gtc ccg cac tgc atc 1548
Ala Glu Ala Val Arg Lys Phe Gly Pro Leu Met Val Pro His Cys Ile
480 485 490 495

55 atc tcc atg gcc tct tcc gtc acg gac atc ctc gaa ccg atg gtc ctc 1596

| Ile | Ser | Met | Ala | Ser | Ser | Val | Thr | Asp | Ile | Leu | Glu | Pro | Met | Val | Leu | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| 500 | | | | 505 | | | | 510 | | | | | | | | |
| ctc | aag | gag | ttc | ggt | ctg | atc | cgg | gcc | aac | ggg | aag | aac | ccg | acg | ggc | 1644 |
| Leu | Lys | Glu | Phe | Gly | Leu | Ile | Arg | Ala | Asn | Gly | Lys | Asn | Pro | Thr | Gly | |
| 515 | | | | 520 | | | | 525 | | | | | | | | |
| agc | gtc | gac | gig | atc | ccg | ctg | ttc | gag | acg | atc | gat | gac | ctc | cag | cgt | 1692 |
| Ser | Val | Asp | Val | Ile | Pro | Leu | Phe | Glu | Thr | Ile | Asp | Asp | Leu | Gln | Arg | |
| 530 | | | | 535 | | | | 540 | | | | | | | | |
| ggc | gcg | ggc | atc | ctg | gag | gaa | tig | igg | gac | atc | gac | ctc | tac | cgc | aal | 1740 |
| Gly | Ala | Gly | Ile | Leu | Glu | Glu | Leu | Trp | Asp | Ile | Asp | Leu | Tyr | Arg | Asn | |
| 545 | | | | 550 | | | | 555 | | | | | | | | |
| tac | ctt | gag | cag | cgg | gac | aac | gtc | cag | gag | gtc | atg | ctg | ggg | tat | tcc | 1788 |
| Tyr | Leu | Glu | Gln | Arg | Asp | Asn | Val | Gln | Glu | Val | Met | Leu | Gly | Tyr | Ser | |
| 560 | 565 | | | | 570 | | | | 575 | | | | | | | |
| gac | tcc | aac | aag | gac | ggc | ggg | tac | ttc | gcc | gcc | aac | igg | gcg | ctt | tac | 1836 |
| Asp | Ser | Asn | Lys | Asp | Gly | Gly | Tyr | Phe | Ala | Ala | Asn | Trp | Ala | Leu | Tyr | |
| 580 | | | | 585 | | | | 590 | | | | | | | | |
| gac | gcg | gag | tta | cgc | ctg | gtc | gaa | cta | tgc | cgg | ggc | cgt | aal | gtc | aag | 1884 |
| Asp | Ala | Glu | Leu | Arg | Leu | Val | Glu | Leu | Cys | Arg | Gly | Arg | Asn | Val | Lys | |
| 595 | | | | 600 | | | | 605 | | | | | | | | |
| ctc | cgt | ctc | ttc | cac | ggt | cgt | ggt | ggc | acg | gtg | ggt | cgt | ggc | ggt | ggc | 1932 |
| Leu | Arg | Leu | Phe | His | Gly | Arg | Gly | Gly | Thr | Val | Gly | Arg | Gly | Gly | Gly | |
| 610 | | | | 615 | | | | 620 | | | | | | | | |
| ccc | tcc | tat | gat | gcg | atc | ctg | gcc | cag | ccc | aag | ggc | gcg | gtc | cgg | ggt | 1980 |
| Pro | Ser | Tyr | Asp | Ala | Ile | Leu | Ala | Gln | Pro | Lys | Gly | Ala | Val | Arg | Gly | |
| 625 | | | | 630 | | | | 635 | | | | | | | | |
| gcg | gtg | cgg | gig | act | gaa | cag | ggc | gag | atc | atc | tcc | gcg | aag | tac | ggt | 2028 |
| Ala | Val | Arg | Val | Thr | Glu | Gln | Gly | Glu | Ile | Ile | Ser | Ala | Lys | Tyr | Gly | |
| 640 | 645 | | | | 650 | | | | 655 | | | | | | | |
| aac | ccg | gat | acg | gca | cgc | cgc | aac | ctt | gag | gcc | ctg | gtg | tcc | gcg | acg | 2076 |
| Asn | Pro | Asp | Thr | Ala | Arg | Arg | Asn | Leu | Glu | Ala | Leu | Val | Ser | Ala | Thr | |
| 660 | | | | 665 | | | | 670 | | | | | | | | |
| ctg | gag | gca | tgc | ctt | ctg | gat | gat | gtg | gaa | ctg | ccc | aal | cgg | gaa | cgc | 2124 |
| Leu | Glu | Ala | Ser | Leu | Leu | Asp | Asp | Val | Glu | Leu | Pro | Asn | Arg | Glu | Arg | |
| 675 | | | | 680 | | | | 685 | | | | | | | | |
| gcg | cac | cag | atc | atg | ggg | gag | atc | tgc | gag | tig | agc | ttc | cgc | agg | tac | 2172 |
| Ala | His | Gln | Ile | Met | Gly | Glu | Ile | Ser | Glu | Leu | Ser | Phe | Arg | Arg | Tyr | |
| 690 | | | | 695 | | | | 700 | | | | | | | | |
| tca | tca | ctg | gtc | cat | gag | gat | ccc | gga | ttc | atc | cag | tac | ttc | acc | cag | 2220 |
| Ser | Ser | Leu | Val | His | Glu | Asp | Pro | Gly | Phe | Ile | Gln | Tyr | Phe | Thr | Gln | |
| 705 | | | | 710 | | | | 715 | | | | | | | | |
| tcc | acc | ccc | ctg | cag | gag | atc | gga | tcc | ctc | aac | atc | ggt | tcc | cga | ccc | 2268 |
| Ser | Thr | Pro | Leu | Gln | Glu | Ile | Gly | Ser | Leu | Asn | Ile | Gly | Ser | Arg | Pro | |

720 725 730 735
 tcc tca cgt aaa cag acc aac acg gtc gag gat ctc cgt gcc atc ccg 2316
 Ser Ser Arg Lys Gln Thr Asn Thr Val Glu Asp Leu Arg Ala Ile Pro
 5 740 745 750
 tgg gtc ctc agc tgg tcc cag tcc cgt gtc atg ctc ccg gcc tgg ttc 2364
 Trp Val Leu Ser Trp Ser Gln Ser Arg Val Met Leu Pro Gly Trp Phe
 10 755 760 765
 ggt gtc ggt acc gca ctc cgt gag tgg atc ggt gag ggc gag ggc gct 2412
 Gly Val Gly Thr Ala Leu Arg Glu Trp Ile Gly Glu Gly Glu Gly Ala
 15 770 775 780
 gcg gag cgc atc gcg gag ctc cag gaa ctc aac cgg tgc tgg ccg ttc 2460
 Ala Glu Arg Ile Ala Glu Leu Gln Glu Leu Asn Arg Cys Trp Pro Phe
 20 785 790 795
 ttc acc tgc gtc ctc gac aac atg gcc cag gtc atg agc aag gcg gaa 2508
 Phe Thr Ser Val Leu Asp Asn Met Ala Gln Val Met Ser Lys Ala Glu
 800 805 810 815
 ctc cgc ctc gcc agc ttc tac gcc gat ctc atc ccg gat cgc gag gtc 2556
 Leu Arg Leu Ala Arg Leu Tyr Ala Asp Leu Ile Pro Asp Arg Glu Val
 25 820 825 830
 gcg gac cgg atc tat gag acc atc ttc ggc gag tat ttc ctc acc aag 2604
 Ala Asp Arg Ile Tyr Glu Thr Ile Phe Gly Glu Tyr Phe Leu Thr Lys
 30 835 840 845
 gag atg ttc tgc acc atc acc ggt tcc cag gac ctc ctc gat gac aac 2652
 Glu Met Phe Cys Thr Ile Thr Gly Ser Gln Asp Leu Leu Asp Asp Asn
 850 855 860
 ccg gcg ctc gcg cga tgc gtc cgc agt cgg ttc ccg tac ctc ctc ccg 2700
 Pro Ala Leu Ala Arg Ser Val Arg Ser Arg Phe Pro Tyr Leu Leu Pro
 35 865 870 875
 ctc aat gtc atc cag gtc gag atg atg cgc cgg tac cgg tcc ggt gat 2748
 Leu Asn Val Ile Gln Val Glu Met Met Arg Arg Tyr Arg Ser Gly Asp
 40 880 885 890 895
 gag ggc acg gct gtc cca cgt aat atc cgc ctc acc atg aat gga ttc 2796
 Glu Gly Thr Ala Val Pro Arg Asn Ile Arg Leu Thr Met Asn Gly Leu
 900 905 910
 45 915
 tcc acg gcc ctc cgc aac tgc ggt tagggcgcca gacgccccgg gaaccgcac 2850
 Ser Thr Ala Leu Arg Asn Ser Gly
 50 915
 ccctgtgtata ctgtctaaag ttgcccggtg tcatccgggc gtgatggata gacaacttaa 2910
 cggcaaagga ttctccccac atggcactga cgtctcaaat cgtctctgtt ctgccagcg 2970
 tgcctatgac ggctctcgtc ctgtctcaca agggtaaggc cggaggctcg tcaagctct 3030
 tgggtggggc cgtccagtc aacctctccg gtccacggg gggtggagaag aacctggacc 3090
 gcgtaccat cctgaccgca gtcctctgtt tgaatctgat tgcgcgtc aacctatcc 3150
 55 915
 aggcgtatc ctgacacctg atctttcaag gccgtccctt cggggcaggc ctcttttgca 3210

ttciccaggt gatgccalc acccaccggt tttaaactat tgaccgatag aaacacctgc 3270
 actaggttat ctgttatgca atagaaaala gtcgal 3306

<210> 26

<211> 919

<212> PRT

<213> Corynebacterium thermoaminogenes

<400> 26

Val Asn Glu Leu Leu Arg Asp Asp Ile Arg Tyr Leu Gly Arg Ile Leu

1 5 10 15

Gly Glu Val Ile Ser Glu Gln Glu Gly His His Val Phe Glu Leu Val

20 25 30

Glu Arg Ala Arg Arg Thr Ser Phe Asp Ile Ala Lys Gly Arg Ala Glu

35 40 45

Met Asp Ser Leu Val Glu Val Phe Ala Gly Ile Asp Pro Glu Asp Ala

50 55 60

Thr Pro Val Ala Arg Ala Phe Thr His Phe Ala Leu Leu Ala Asn Leu

65 70 75 80

Ala Glu Asp Leu His Asp Ala Ala Gln Arg Glu Gln Ala Leu Asn Ser

85 90 95

Gly Glu Pro Ala Pro Asp Ser Thr Leu Glu Ala Thr Trp Val Lys Leu

100 105 110

Asp Asp Ala Gly Val Gly Ser Gly Glu Val Ala Ala Val Ile Arg Asn

115 120 125

Ala Leu Val Ala Pro Val Leu Thr Ala His Pro Thr Glu Thr Arg Arg

130 135 140

Arg Thr Val Phe Asp Ala Gln Lys His Ile Thr Ala Leu Met Glu Glu

145 150 155 160

Arg His Leu Leu Leu Ala Leu Pro Thr His Ala Arg Thr Gln Ser Lys

165 170 175

Leu Asp Asp Ile Glu Arg Asn Ile Arg Arg Arg Ile Thr Ile Leu Trp

180 185 190

Gln Thr Ala Leu Ile Arg Val Ala Arg Pro Arg Ile Glu Asp Glu Val

195 200 205

Glu Val Gly Leu Arg Tyr Tyr Lys Leu Ser Leu Leu Ala Glu Ile Pro

210 215 220

Arg Ile Asn His Asp Val Thr Val Glu Leu Ala Arg Arg Phe Gly Gly

225 230 235 240

Asp Ile Pro Thr Thr Ala Met Val Arg Pro Gly Ser Trp Ile Gly Gly

245 250 255

Asp His Asp Gly Asn Pro Phe Val Thr Ala Glu Thr Val Thr Tyr Ala

260 265 270

Thr His Arg Ala Ala Glu Thr Val Leu Lys Tyr Tyr Val Lys Gln Leu
 275 280 285
 5 His Ala Leu Glu His Glu Leu Ser Leu Ser Asp Arg Met Asn Val Ile
 290 295 300
 Ser Asp Glu Leu Arg Val Leu Ala Asp Ala Gly Gln Asn Asp Met Pro
 305 310 315 320
 10 Ser Arg Val Asp Glu Pro Tyr Arg Arg Ala Ile His Gly Met Arg Gly
 325 330 335
 Arg Met Leu Ala Thr Thr Ala Ala Leu Ile Gly Glu Glu Ala Val Glu
 340 345 350
 15 Gly Thr Trp Phe Lys Thr Phe Thr Pro Tyr Thr Asp Thr His Glu Phe
 355 360 365
 Lys Arg Asp Leu Asp Ile Val Asp Gly Ser Leu Arg Met Ser Arg Asp
 370 375 380
 20 Asp Ile Ile Ala Asp Asp Arg Leu Ala Met Leu Arg Ser Ala Leu Asp
 385 390 395 400
 Ser Phe Gly Phe Asn Leu Tyr Ser Leu Asp Leu Arg Gln Asn Ser Asp
 405 410 415
 25 Gly Phe Glu Asp Val Leu Thr Glu Leu Phe Ala Thr Ala Gln Thr Glu
 420 425 430
 Lys Asn Tyr Arg Gly Leu Thr Glu Ala Glu Lys Leu Asp Leu Leu Ile
 435 440 445
 30 Arg Glu Leu Ser Thr Pro Arg Pro Leu Ile Pro His Gly Asp Pro Asp
 450 455 460
 Tyr Ser Glu Ala Thr Asn Arg Glu Leu Gly Ile Phe Ser Lys Ala Ala
 465 470 475 480
 35 Glu Ala Val Arg Lys Phe Gly Pro Leu Met Val Pro His Cys Ile Ile
 485 490 495
 Ser Met Ala Ser Ser Val Thr Asp Ile Leu Glu Pro Met Val Leu Leu
 500 505 510
 40 Lys Glu Phe Gly Leu Ile Arg Ala Asn Gly Lys Asn Pro Thr Gly Ser
 515 520 525
 Val Asp Val Ile Pro Leu Phe Glu Thr Ile Asp Asp Leu Gln Arg Gly
 530 535 540
 45 Ala Gly Ile Leu Glu Glu Leu Trp Asp Ile Asp Leu Tyr Arg Asn Tyr
 545 550 555 560
 Leu Glu Gln Arg Asp Asn Val Gln Glu Val Met Leu Gly Tyr Ser Asp
 565 570 575
 50 Ser Asn Lys Asp Gly Gly Tyr Phe Ala Ala Asn Trp Ala Leu Tyr Asp
 580 585 590
 Ala Glu Leu Arg Leu Val Glu Leu Cys Arg Gly Arg Asn Val Lys Leu
 595 600 605
 55 Arg Leu Phe His Gly Arg Gly Gly Thr Val Gly Arg Gly Gly Gly Pro

| | | | | | | |
|----|---|---|-----|-----|-----|--|
| | 610 | | 615 | | 620 | |
| | Ser Tyr Asp Ala Ile Leu | Ala Gln Pro Lys Gly Ala Val Arg Gly Ala | | | | |
| 5 | 625 | 630 | 635 | 640 | | |
| | Val Arg Val Thr Glu Gln Gly Glu Ile Ile Ser Ala Lys Tyr Gly Asn | | | | | |
| | | 645 | 650 | 655 | | |
| | Pro Asp Thr Ala Arg Arg Asn Leu Glu Ala Leu Val Ser Ala Thr Leu | | | | | |
| 10 | | 660 | 665 | 670 | | |
| | Glu Ala Ser Leu Leu Asp Asp Val Glu Leu Pro Asn Arg Glu Arg Ala | | | | | |
| | | 675 | 680 | 685 | | |
| | His Gln Ile Met Gly Glu Ile Ser Glu Leu Ser Phe Arg Arg Tyr Ser | | | | | |
| 15 | | 690 | 695 | 700 | | |
| | Ser Leu Val His Glu Asp Pro Gly Phe Ile Gln Tyr Phe Thr Gln Ser | | | | | |
| | 705 | 710 | 715 | 720 | | |
| | Thr Pro Leu Gln Glu Ile Gly Ser Leu Asn Ile Gly Ser Arg Pro Ser | | | | | |
| 20 | | 725 | 730 | 735 | | |
| | Ser Arg Lys Gln Thr Asn Thr Val Glu Asp Leu Arg Ala Ile Pro Trp | | | | | |
| | | 740 | 745 | 750 | | |
| | Val Leu Ser Trp Ser Gln Ser Arg Val Met Leu Pro Gly Trp Phe Gly | | | | | |
| 25 | | 755 | 760 | 765 | | |
| | Val Gly Thr Ala Leu Arg Glu Trp Ile Gly Glu Gly Glu Gly Ala Ala | | | | | |
| | | 770 | 775 | 780 | | |
| | Glu Arg Ile Ala Glu Leu Gln Glu Leu Asn Arg Cys Trp Pro Phe Phe | | | | | |
| 30 | | 785 | 790 | 795 | 800 | |
| | Thr Ser Val Leu Asp Asn Met Ala Gln Val Met Ser Lys Ala Glu Leu | | | | | |
| | | 805 | 810 | 815 | | |
| | Arg Leu Ala Arg Leu Tyr Ala Asp Leu Ile Pro Asp Arg Glu Val Ala | | | | | |
| 35 | | 820 | 825 | 830 | | |
| | Asp Arg Ile Tyr Glu Thr Ile Phe Gly Glu Tyr Phe Leu Thr Lys Glu | | | | | |
| | | 835 | 840 | 845 | | |
| | Met Phe Cys Thr Ile Thr Gly Ser Gln Asp Leu Leu Asp Asp Asn Pro | | | | | |
| 40 | | 850 | 855 | 860 | | |
| | Ala Leu Ala Arg Ser Val Arg Ser Arg Phe Pro Tyr Leu Leu Pro Leu | | | | | |
| | | 865 | 870 | 875 | 880 | |
| | Asn Val Ile Gln Val Glu Met Met Arg Arg Tyr Arg Ser Gly Asp Glu | | | | | |
| 45 | | 885 | 890 | 895 | | |
| | Gly Thr Ala Val Pro Arg Asn Ile Arg Leu Thr Met Asn Gly Leu Ser | | | | | |
| | | 900 | 905 | 910 | | |
| | Thr Ala Leu Arg Asn Ser Gly | | | | | |
| 50 | | 915 | | | | |

<210> 27

<211> 3907

<212> DNA

<213> *Corynebacterium thermoaminogenes*

<220>

<221> CDS

<222> (686)..(3388)

<400> 27

attacttcag ctgactcagc aacattcgta ttaggtatgc aaacaacatt. tggltcgtaa 60
 aatccaagta gtaaggtaa agtaacttgg ggtatgcgc aagcacatat cgccttltga 120
 ttattattag ctggggcgga agatggaact aaagctctca acgcaattca gaglgccgct 180
 attattagtg cgtttccatt ctcctttgtc gtcataataa tgaatgacag ttcttacaata 240
 galgctaata aagaacgtaa attcttagga ttaacattaa cgcttaataa acacagattaa 300
 gaagaatacg ttaataatca acaagaggat tacgaatcgc atattttaga aaaacgtgaa 360
 tctagacgtg atcgtgaaag agaagaataa ttgaatgaaa tatctactat aatgggtgggt 420
 ttaaagctat caacaatttt gtgatagct attttatgt ttaacaataa taaatattat 480
 ttacttgcga ttgataacca ttctcaatta ataaaaataa cttatagtac aaatgcgtta 540
 taataagttt tacttatact accgatataa aaatgcgaaa tgaataatga cccctttata 600
 tacttataca gtgtgttcg aaaacatata ataatacaat ttaactaagg catataaata 660
 tatagaaatt caagggggat atcaa atg gct tct aat ttt aaa gaa aca gcg 712
 Met Ala Ser Asn Phe Lys Glu Thr Ala
 1 5
 aag aaa caa ttt gat tta aat ggc caa tca tac acg tac tat gat tta 760
 Lys Lys Gln Phe Asp Leu Asn Gly Gln Ser Tyr Thr Tyr Tyr Asp Leu
 10 15 20 25
 aaa tca tta gaa gaa caa ggt tta act aaa att tca aag tta cct tat 808
 Lys Ser Leu Glu Glu Gln Gly Leu Thr Lys Ile Ser Lys Leu Pro Tyr
 30 35 40
 tca atc cgt gta tta cta gaa tca gtg tta cgt cag gaa gat gat ttt 856
 Ser Ile Arg Val Leu Leu Glu Ser Val Leu Arg Gln Glu Asp Asp Phe
 45 50 55
 gla att act gat gat cac att aaa caa tta gca gaa ttt ggc aaa aaa 904
 Val Ile Thr Asp Asp His Ile Lys Gln Leu Ala Glu Phe Gly Lys Lys
 60 65 70
 ggt aac gaa ggt gaa gta cct ttc aaa cca tct cga gtt att tta caa 952
 Gly Asn Glu Gly Glu Val Pro Phe Lys Pro Ser Arg Val Ile Leu Gln
 75 80 85
 gac ttc act ggt gta cca gca gla gtt gac tta gcg tct tta cgt aaa 1000
 Asp Phe Thr Gly Val Pro Ala Val Val Asp Leu Ala Ser Leu Arg Lys
 90 95 100 105
 gca atg aat gat gtt ggt ggg gat att aat aaa att aac cct gaa gla 1048
 Ala Met Asn Asp Val Gly Gly Asp Ile Asn Lys Ile Asn Pro Glu Val
 110 115 120
 cca gtt gac tta gtt att gac cac tct gla caa gla gat agt tat gct 1096

Pro Val Asp Leu Val Ile Asp His Ser Val Gln Val Asp Ser Tyr Ala

125

130

135

| | | |
|----|---|------|
| 5 | aal cca gat gca tta caa cgt aac atg aaa tta gaa ttt gaa cgt aac | 1144 |
| | Asn Pro Asp Ala Leu Gln Arg Asn Met Lys Leu Glu Phe Glu Arg Asn | |
| | 140 145 150 | |
| 10 | tat gaa cgt tac caa ttc tta aac tgg gca aca aaa gca ttt gat aac | 1192 |
| | Tyr Glu Arg Tyr Gln Phe Leu Asn Trp Ala Thr Lys Ala Phe Asp Asn | |
| | 155 160 165 | |
| 15 | tat aat gca gta cca cct gct aca ggt att gtc cac caa gta aac tta | 1240 |
| | Tyr Asn Ala Val Pro Pro Ala Thr Gly Ile Val His Gln Val Asn Leu | |
| | 170 175 180 185 | |
| | gaa tac tta gcg aat gtt gta cat gtt cgt gac gtt gac gga gaa caa | 1288 |
| | Glu Tyr Leu Ala Asn Val Val His Val Arg Asp Val Asp Gly Glu Gln | |
| | 190 195 200 | |
| 20 | act gct ttc cca gat aca tta gtt ggt act gac tca cat act aca atg | 1336 |
| | Thr Ala Phe Pro Asp Thr Leu Val Gly Thr Asp Ser His Thr Thr Met | |
| | 205 210 215 | |
| 25 | att aac ggt att ggt gta tta ggt tgg ggt gtc ggc ggt atc gaa gct | 1384 |
| | Ile Asn Gly Ile Gly Val Leu Gly Trp Gly Val Gly Gly Ile Glu Ala | |
| | 220 225 230 | |
| 30 | gaa gca ggt atg tta gga caa cca tca tac ttc cca att cca gaa gtt | 1432 |
| | Glu Ala Gly Met Leu Gly Gln Pro Ser Tyr Phe Pro Ile Pro Glu Val | |
| | 235 240 245 | |
| | att ggt gtt aaa tta agt aat gaa tta cca caa ggt tca aca gca act | 1480 |
| | Ile Gly Val Lys Leu Ser Asn Glu Leu Pro Gln Gly Ser Thr Ala Thr | |
| | 250 255 260 265 | |
| 35 | gac tta gca tta cgt gla act gaa gag tta cgt aaa cgt ggt gla gla | 1528 |
| | Asp Leu Ala Leu Arg Val Thr Glu Glu Leu Arg Lys Arg Gly Val Val | |
| | 270 275 280 | |
| 40 | ggt aaa ttc gtt gag ttc ttt ggt cct ggt gla aca aac tta cca tta | 1576 |
| | Gly Lys Phe Val Glu Phe Phe Gly Pro Gly Val Thr Asn Leu Pro Leu | |
| | 285 290 295 | |
| | gct gac cgt gca aca att gcg aac atg gcg cct gaa tat ggt gca act | 1624 |
| | Ala Asp Arg Ala Thr Ile Ala Asn Met Ala Pro Glu Tyr Gly Ala Thr | |
| 45 | 300 305 310 | |
| | tgt ggt ttc ttc cca gtt gat gaa gaa tca ctt aaa tac atg aaa tta | 1672 |
| | Cys Gly Phe Phe Pro Val Asp Glu Glu Ser Leu Lys Tyr Met Lys Leu | |
| | 315 320 325 | |
| 50 | act ggt cgt aaa gat gat cat att gca cia gla aaa gaa tat tta caa | 1720 |
| | Thr Gly Arg Lys Asp Asp His Ile Ala Leu Val Lys Glu Tyr Leu Gln | |
| | 330 335 340 345 | |
| 55 | caa aat aat atg ttc ttc caa gtt gaa aat gaa gat cct gaa tat act | 1768 |
| | Gln Asn Asn Met Phe Phe Gln Val Glu Asn Glu Asp Pro Glu Tyr Thr | |

| | | | | |
|----|---|------|-----|--|
| | 350 | 355 | 360 | |
| | gaa gtg att gat tta gat tta tct aca gtt caa gct tct tta tca ggt | 1816 | | |
| 5 | Glu Val Ile Asp Leu Asp Leu Ser Thr Val Gln Ala Ser Leu Ser Gly | | | |
| | 365 370 375 | | | |
| | cca aaa cgt cca caa gat tta atc ttc tta agt gac atg aaa act gaa | 1864 | | |
| | Pro Lys Arg Pro Gln Asp Leu Ile Phe Leu Ser Asp Met Lys Thr Glu | | | |
| 10 | 380 385 390 | | | |
| | ttc gaa aaa tca gtt aca gca cca gct ggt aac caa ggt cac ggt tta | 1912 | | |
| | Phe Glu Lys Ser Val Thr Ala Pro Ala Gly Asn Gln Gly His Gly Leu | | | |
| | 395 400 405 | | | |
| 15 | gat gaa agt gaa ttt gat aag aaa gca gaa atc aaa ttt aat gat ggt | 1960 | | |
| | Asp Glu Ser Glu Phe Asp Lys Lys Ala Glu Ile Lys Phe Asn Asp Gly | | | |
| | 410 415 420 425 | | | |
| 20 | aga act tca act atg aag act ggt gat gtt gcg att gca gcg att aca | 2008 | | |
| | Arg Thr Ser Thr Met Lys Thr Gly Asp Val Ala Ile Ala Ala Ile Thr | | | |
| | 430 435 440 | | | |
| | tca tgt aca aat aca tct aac cct tac gtt atg tta ggt gca ggt tta | 2056 | | |
| | Ser Cys Thr Asn Thr Ser Asn Pro Tyr Val Met Leu Gly Ala Gly Leu | | | |
| 25 | 445 450 455 | | | |
| | gia gct aaa aaa gca att gaa aaa ggc tta aaa gia cct gat tat gia | 2104 | | |
| | Val Ala Lys Lys Ala Ile Glu Lys Gly Leu Lys Val Pro Asp Tyr Val | | | |
| | 460 465 470 | | | |
| 30 | aaa act tca tta gca cca ggt tca aaa gtt gtt act gga tat tta aga | 2152 | | |
| | Lys Thr Ser Leu Ala Pro Gly Ser Lys Val Val Thr Gly Tyr Leu Arg | | | |
| | 475 480 485 | | | |
| 35 | gat tca ggt tta caa gaa tat ctt gat gac tta ggt ttc aac tta gtt | 2200 | | |
| | Asp Ser Gly Leu Gln Glu Tyr Leu Asp Asp Leu Gly Phe Asn Leu Val | | | |
| | 490 495 500 505 | | | |
| | ggt tat ggt tgt aca act tgt atc ggt aac tca ggt cca tta tta cct | 2248 | | |
| | Gly Tyr Gly Cys Thr Thr Cys Ile Gly Asn Ser Gly Pro Leu Leu Pro | | | |
| 40 | 510 515 520 | | | |
| | gaa att gaa aaa gca gia gct gac gaa gat tta tta gia act tct gia | 2296 | | |
| | Glu Ile Glu Lys Ala Val Ala Asp Glu Asp Leu Leu Val Thr Ser Val | | | |
| | 525 530 535 | | | |
| 45 | ctt tct ggt aac cgt aac ttt gaa ggt cgt atc cat ccg tta gtt aaa | 2344 | | |
| | Leu Ser Gly Asn Arg Asn Phe Glu Gly Arg Ile His Pro Leu Val Lys | | | |
| | 540 545 550 | | | |
| 50 | gct aac tac tta gct tca cca caa tta gtt gia gct tat gca tta gct | 2392 | | |
| | Ala Asn Tyr Leu Ala Ser Pro Gln Leu Val Val Ala Tyr Ala Leu Ala | | | |
| | 555 560 565 | | | |
| | gga acg gtt gat atc gat tta cac aat gaa cct atc ggt aaa ggt aaa | 2440 | | |
| 55 | Gly Thr Val Asp Ile Asp Leu His Asn Glu Pro Ile Gly Lys Gly Lys | | | |
| | 570 575 580 585 | | | |

EP 1 219 712 A1

| | | | | | | | | | | | | | | | | | |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| | gat | ggc | gaa | gat | gta | tac | ctt | aaa | gat | atc | tgg | cca | agt | atc | aaa | gaa | 2488 |
| | Asp | Gly | Glu | Asp | Val | Tyr | Leu | Lys | Asp | Ile | Trp | Pro | Ser | Ile | Lys | Glu | |
| | | | | 590 | | | | | 595 | | | | | | 600 | | |
| 5 | gtt | gca | gac | act | gtt | gat | agt | gtc | gta | acg | cca | gaa | tta | ttc | tta | gaa | 2536 |
| | Val | Ala | Asp | Thr | Val | Asp | Ser | Val | Val | Thr | Pro | Glu | Leu | Phe | Leu | Glu | |
| | | | | 605 | | | | | 610 | | | | | | 615 | | |
| 10 | gaa | tat | gca | aat | gta | tac | gaa | aat | aat | gaa | atg | tgg | aat | gaa | atc | gac | 2584 |
| | Glu | Tyr | Ala | Asn | Val | Tyr | Glu | Asn | Asn | Glu | Met | Trp | Asn | Glu | Ile | Asp | |
| | | | | 620 | | | | | 625 | | | | | | 630 | | |
| 15 | gtt | act | gac | gca | cca | tta | tat | gat | ttc | gat | cca | aat | tca | act | tat | att | 2632 |
| | Val | Thr | Asp | Ala | Pro | Leu | Tyr | Asp | Phe | Asp | Pro | Asn | Ser | Thr | Tyr | Ile | |
| | | | | 635 | | | | | 640 | | | | | | 645 | | |
| 20 | caa | aat | cca | tca | ttc | ttc | caa | ggt | tta | lct | aaa | gaa | cca | gga | act | att | 2680 |
| | Gln | Asn | Pro | Ser | Phe | Phe | Gln | Gly | Leu | Ser | Lys | Glu | Pro | Gly | Thr | Ile | |
| | | | | 650 | | | | | 655 | | | | | | 660 | | |
| 25 | gaa | cca | tta | aaa | gat | tta | cgt | att | atg | ggt | aaa | ttt | ggt | gat | tca | gtt | 2728 |
| | Glu | Pro | Leu | Lys | Asp | Leu | Arg | Ile | Met | Gly | Lys | Phe | Gly | Asp | Ser | Val | |
| | | | | | 670 | | | | | 675 | | | | | 680 | | |
| 30 | aca | act | gac | cac | att | lct | cca | gca | ggt | gcg | atc | ggt | aaa | gat | aca | cca | 2776 |
| | Thr | Thr | Asp | His | Ile | Ser | Pro | Ala | Gly | Ala | Ile | Gly | Lys | Asp | Thr | Pro | |
| | | | | 685 | | | | | 690 | | | | | | 695 | | |
| 35 | gca | ggt | aaa | tat | tta | tta | gac | cat | gat | gtt | cca | att | aga | gaa | ttt | aac | 2824 |
| | Ala | Gly | Lys | Tyr | Leu | Leu | Asp | His | Asp | Val | Pro | Ile | Arg | Glu | Phe | Asn | |
| | | | | 700 | | | | | 705 | | | | | | 710 | | |
| 40 | tct | tat | ggt | tca | aga | cgt | ggt | aac | cat | gaa | gta | atg | gta | cgt | ggt | act | 2872 |
| | Ser | Tyr | Gly | Ser | Arg | Arg | Gly | Asn | His | Glu | Val | Met | Val | Arg | Gly | Thr | |
| | | | | 715 | | | | | 720 | | | | | | 725 | | |
| 45 | ttc | gct | aat | atc | cgt | att | aaa | aac | caa | tta | gca | cca | ggc | act | gaa | ggt | 2920 |
| | Phe | Ala | Asn | Ile | Arg | Ile | Lys | Asn | Gln | Leu | Ala | Pro | Gly | Thr | Glu | Gly | |
| | | | | 730 | | | | | 735 | | | | | | 740 | | |
| 50 | gga | ttt | aca | aca | tat | tgg | cct | aca | gaa | gaa | atc | atg | cct | atc | tat | gat | 2968 |
| | Gly | Phe | Thr | Thr | Tyr | Trp | Pro | Thr | Glu | Glu | Ile | Met | Pro | Ile | Tyr | Asp | |
| | | | | | 750 | | | | 755 | | | | | | 760 | | |
| 55 | gca | gct | atg | aga | tac | aaa | gaa | aat | ggt | act | ggt | tta | gct | gtt | tta | gct | 3016 |
| | Ala | Ala | Met | Arg | Tyr | Lys | Glu | Asn | Gly | Thr | Gly | Leu | Ala | Val | Leu | Ala | |
| | | | | 765 | | | | | 770 | | | | | | 775 | | |
| 60 | ggt | aat | gat | tac | ggt | atg | ggt | tca | lct | cgt | gac | tgg | gca | gct | aaa | ggt | 3064 |
| | Gly | Asn | Asp | Tyr | Gly | Met | Gly | Ser | Ser | Arg | Asp | Trp | Ala | Ala | Lys | Gly | |
| | | | | 780 | | | | | 785 | | | | | | 790 | | |
| 65 | act | aac | tta | tta | ggt | gtt | aaa | act | gtt | att | gca | caa | agt | tat | gaa | cgt | 3112 |
| | Thr | Asn | Leu | Leu | Gly | Val | Lys | Thr | Val | Ile | Ala | Gln | Ser | Tyr | Glu | Arg | |
| | | | | 795 | | | | | 800 | | | | | | 805 | | |
| 70 | atc | cat | cgt | tca | aac | tta | gta | atg | atg | ggt | gta | tta | cca | tta | caa | ttt | 3160 |

11e His Arg Ser Asn Leu Val Met Met Gly Val Leu Pro Leu Gln Phe
 810 815 820 825
 5 aaa caa ggt gag tca gct gat tct cta ggt tta gaa ggt aaa gaa gaa 3208
 Lys Gln Gly Glu Ser Ala Asp Ser Leu Gly Leu Glu Gly Lys Glu Glu
 830 835 840
 10 att tct gla gat atc gat gaa aat gtt aaa cca cat gat tta gla act 3256
 Ile Ser Val Asp Ile Asp Glu Asn Val Lys Pro His Asp Leu Val Thr
 845 850 855
 gtt cat gct aaa aaa gaa aac gga gaa gtt gtt gat ttt gaa gca atg 3304
 Val His Ala Lys Lys Glu Asn Gly Glu Val Val Asp Phe Glu Ala Met
 860 865 870
 15 gtt cgt ttc gat tca tta gla gaa tta gat tat tat cgt cat ggt ggt 3352
 Val Arg Phe Asp Ser Leu Val Glu Leu Asp Tyr Tyr Arg His Gly Gly
 875 880 885
 20 atc tta caa atg gta tta aga aac aaa tta gct caa taatcacaat 3398
 Ile Leu Gln Met Val Leu Arg Asn Lys Leu Ala Gln
 890 895 900
 25 gtgacttttg acagtgctaa cgtttagggt agcacgtttt ttttatgcta aactatata 3458
 gtaagttaa tagttaagga aggatggac ttaaagtatt tatagtttga ctgaaatiga 3518
 accaagatat caagagacag alaaaatggg cgtgatttat calggcaatt atgcaacalg 3578
 gtttgaagta gcgcgtacag attacattag aaaactlagga tttagttatg ctgatatgga 3638
 aaagcaaggg aicatttcic cagttacaga cttaaatatc aaatataaaa aatcaatttt 3698
 30 ttatccigaa aaagtaacca ttaaaacatg ggttgaaaaa tattcaagal tacgttcigi 3758
 gtatagatat gaaattttta algaacaggg agaactigca actacagggt alactgagtt 3818
 aatttgtaig aaagcigata cctttagacc aattagattt gatcgttatt tctcagattg 3878
 gcatgaaacc tatagtaaag tgaagctt 3907
 35
 <210> 28
 <211> 901
 <212> PRT
 40 <213> Corynebacterium thermoaminogenes
 <400> 28
 45 Met Ala Ser Asn Phe Lys Glu Thr Ala Lys Lys Gln Phe Asp Leu Asn
 1 5 10 15
 Gly Gln Ser Tyr Thr Tyr Tyr Asp Leu Lys Ser Leu Glu Glu Gln Gly
 20 25 30
 50 Leu Thr Lys Ile Ser Lys Leu Pro Tyr Ser Ile Arg Val Leu Leu Glu
 35 40 45
 Ser Val Leu Arg Gln Glu Asp Asp Phe Val Ile Thr Asp Asp His Ile
 50 55 60
 55 Lys Gln Leu Ala Glu Phe Gly Lys Lys Gly Asn Glu Gly Glu Val Pro
 65 70 75 80

| | | | | | | | | | | | | | | | | |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| | Phe | Lys | Pro | Ser | Arg | Val | Ile | Leu | Gln | Asp | Phe | Thr | Gly | Val | Pro | Ala |
| | | | | | 85 | | | | | 90 | | | | | 95 | |
| 5 | Val | Val | Asp | Leu | Ala | Ser | Leu | Arg | Lys | Ala | Met | Asn | Asp | Val | Gly | Gly |
| | | | | 100 | | | | | 105 | | | | | 110 | | |
| | Asp | Ile | Asn | Lys | Ile | Asn | Pro | Glu | Val | Pro | Val | Asp | Leu | Val | Ile | Asp |
| | | | 115 | | | | | 120 | | | | | 125 | | | |
| 10 | His | Ser | Val | Gln | Val | Asp | Ser | Tyr | Ala | Asn | Pro | Asp | Ala | Leu | Gln | Arg |
| | | 130 | | | | | 135 | | | | 140 | | | | | |
| | Asn | Met | Lys | Leu | Glu | Phe | Glu | Arg | Asn | Tyr | Glu | Arg | Tyr | Gln | Phe | Leu |
| | 145 | | | | 150 | | | | | 155 | | | | | 160 | |
| 15 | Asn | Trp | Ala | Thr | Lys | Ala | Phe | Asp | Asn | Tyr | Asn | Ala | Val | Pro | Pro | Ala |
| | | | | 165 | | | | | 170 | | | | | 175 | | |
| | Thr | Gly | Ile | Val | His | Gln | Val | Asn | Leu | Glu | Tyr | Leu | Ala | Asn | Val | Val |
| | | | 180 | | | | | 185 | | | | | | 190 | | |
| 20 | His | Val | Arg | Asp | Val | Asp | Gly | Glu | Gln | Thr | Ala | Phe | Pro | Asp | Thr | Leu |
| | | 195 | | | | | | 200 | | | | 205 | | | | |
| | Val | Gly | Thr | Asp | Ser | His | Thr | Thr | Met | Ile | Asn | Gly | Ile | Gly | Val | Leu |
| | | 210 | | | | | 215 | | | | | 220 | | | | |
| 25 | Gly | Trp | Gly | Val | Gly | Gly | Ile | Glu | Ala | Glu | Ala | Gly | Met | Leu | Gly | Gln |
| | 225 | | | | 230 | | | | | 235 | | | | | 240 | |
| | Pro | Ser | Tyr | Phe | Pro | Ile | Pro | Glu | Val | Ile | Gly | Val | Lys | Leu | Ser | Asn |
| | | | | 245 | | | | | 250 | | | | | 255 | | |
| 30 | Glu | Leu | Pro | Gln | Gly | Ser | Thr | Ala | Thr | Asp | Leu | Ala | Leu | Arg | Val | Thr |
| | | | 260 | | | | | 265 | | | | | | 270 | | |
| | Glu | Glu | Leu | Arg | Lys | Arg | Gly | Val | Val | Gly | Lys | Phe | Val | Glu | Phe | Phe |
| | | 275 | | | | | 280 | | | | | 285 | | | | |
| 35 | Gly | Pro | Gly | Val | Thr | Asn | Leu | Pro | Leu | Ala | Asp | Arg | Ala | Thr | Ile | Ala |
| | 290 | | | | | 295 | | | | | 300 | | | | | |
| | Asn | Met | Ala | Pro | Glu | Tyr | Gly | Ala | Thr | Cys | Gly | Phe | Phe | Pro | Val | Asp |
| | 305 | | | | 310 | | | | | 315 | | | | | 320 | |
| 40 | Glu | Glu | Ser | Leu | Lys | Tyr | Met | Lys | Leu | Thr | Gly | Arg | Lys | Asp | Asp | His |
| | | | 325 | | | | | | 330 | | | | | 335 | | |
| | Ile | Ala | Leu | Val | Lys | Glu | Tyr | Leu | Gln | Gln | Asn | Asn | Met | Phe | Phe | Gln |
| | | 340 | | | | | | 345 | | | | | 350 | | | |
| 45 | Val | Glu | Asn | Glu | Asp | Pro | Glu | Tyr | Thr | Glu | Val | Ile | Asp | Leu | Asp | Leu |
| | | 355 | | | | | 360 | | | | | | 365 | | | |
| | Ser | Thr | Val | Gln | Ala | Ser | Leu | Ser | Gly | Pro | Lys | Arg | Pro | Gln | Asp | Leu |
| | | 370 | | | | 375 | | | | | 380 | | | | | |
| 50 | Ile | Phe | Leu | Ser | Asp | Met | Lys | Thr | Glu | Phe | Glu | Lys | Ser | Val | Thr | Ala |
| | 385 | | | | 390 | | | | | 395 | | | | | 400 | |
| | Pro | Ala | Gly | Asn | Gln | Gly | His | Gly | Leu | Asp | Glu | Ser | Glu | Phe | Asp | Lys |
| | | | | 405 | | | | 410 | | | | | 415 | | | |
| 55 | Lys | Ala | Glu | Ile | Lys | Phe | Asn | Asp | Gly | Arg | Thr | Ser | Thr | Met | Lys | Thr |

420 425 430
 Gly Asp Val Ala Ile Ala Ala Ile Thr Ser Cys Thr Asn Thr Ser Asn
 435 440 445
 5 Pro Tyr Val Met Leu Gly Ala Gly Leu Val Ala Lys Lys Ala Ile Glu
 450 455 460
 Lys Gly Leu Lys Val Pro Asp Tyr Val Lys Thr Ser Leu Ala Pro Gly
 10 465 470 475 480
 Ser Lys Val Val Thr Gly Tyr Leu Arg Asp Ser Gly Leu Gln Glu Tyr
 485 490 495
 Leu Asp Asp Leu Gly Phe Asn Leu Val Gly Tyr Gly Cys Thr Thr Cys
 15 500 505 510
 Ile Gly Asn Ser Gly Pro Leu Leu Pro Glu Ile Glu Lys Ala Val Ala
 515 520 525
 Asp Glu Asp Leu Leu Val Thr Ser Val Leu Ser Gly Asn Arg Asn Phe
 20 530 535 540
 Glu Gly Arg Ile His Pro Leu Val Lys Ala Asn Tyr Leu Ala Ser Pro
 545 550 555 560
 Gln Leu Val Val Ala Tyr Ala Leu Ala Gly Thr Val Asp Ile Asp Leu
 25 565 570 575
 His Asn Glu Pro Ile Gly Lys Gly Lys Asp Gly Glu Asp Val Tyr Leu
 580 585 590
 Lys Asp Ile Trp Pro Ser Ile Lys Glu Val Ala Asp Thr Val Asp Ser
 30 595 600 605
 Val Val Thr Pro Glu Leu Phe Leu Glu Glu Tyr Ala Asn Val Tyr Glu
 610 615 620
 Asn Asn Glu Met Trp Asn Glu Ile Asp Val Thr Asp Ala Pro Leu Tyr
 35 625 630 635 640
 Asp Phe Asp Pro Asn Ser Thr Tyr Ile Gln Asn Pro Ser Phe Phe Gln
 645 650 655
 Gly Leu Ser Lys Glu Pro Gly Thr Ile Glu Pro Leu Lys Asp Leu Arg
 40 660 665 670
 Ile Met Gly Lys Phe Gly Asp Ser Val Thr Thr Asp His Ile Ser Pro
 675 680 685
 Ala Gly Ala Ile Gly Lys Asp Thr Pro Ala Gly Lys Tyr Leu Leu Asp
 45 690 695 700
 His Asp Val Pro Ile Arg Glu Phe Asn Ser Tyr Gly Ser Arg Arg Gly
 705 710 715 720
 Asn His Glu Val Met Val Arg Gly Thr Phe Ala Asn Ile Arg Ile Lys
 50 725 730 735
 Asn Gln Leu Ala Pro Gly Thr Glu Gly Gly Phe Thr Thr Tyr Trp Pro
 740 745 750
 55 Thr Glu Glu Ile Met Pro Ile Tyr Asp Ala Ala Met Arg Tyr Lys Glu
 755 760 765

Asn Gly Thr Gly Leu Ala Val Leu Ala Gly Asn Asp Tyr Gly Met Gly
770 775 780

Ser Ser Arg Asp Trp Ala Ala Lys Gly Thr Asn Leu Leu Gly Val Lys
785 790 795 800

Thr Val Ile Ala Gln Ser Tyr Glu Arg Ile His Arg Ser Asn Leu Val
805 810 815

Met Met Gly Val Leu Pro Leu Gln Phe Lys Gln Gly Glu Ser Ala Asp
820 825 830

Ser Leu Gly Leu Glu Gly Lys Glu Glu Ile Ser Val Asp Ile Asp Glu
835 840 845

Asn Val Lys Pro His Asp Leu Val Thr Val His Ala Lys Lys Glu Asn
850 855 860

Gly Glu Val Val Asp Phe Glu Ala Met Val Arg Phe Asp Ser Leu Val
865 870 875 880

Glu Leu Asp Tyr Tyr Arg His Gly Gly Ile Leu Gln Met Val Leu Arg
885 890 895

Asn Lys Leu Ala Gln
900

<210> 29

<211> 3006

<212> DNA

<213> *Corynebacterium thermoaminogenes*

<220>

<221> CDS

<222> (328).. (2514)

<400> 29

gicgacgacg aacccccac cgccgaacca gccgccgac tgggtgggga gacacccggg 60

lclclclccc lgggtgaaca ggtgccacaa ccccgcccc acaggcacac ctaccacigg 120

alcgccgggg agagcagcat ggicacacgc clgcggcgig cccgggggaa ggalcacggc 180

ciggacagat cgcaggiggg alicatgggi latggagggc agggaglggc calgaggggi 240

lgatalcgcl lcccgagggg lccgcaggcg lgcclacccc lgtatcttg atagtigaac 300

aaaagagccc acataacaag gagatic alg gcl aag atc atc lgg acc cgc acc 354

Met Ala Lys Ile Ile Trp Thr Arg Thr

1

5

gac gaa gca ccg clg clc gcg acc tac tgc clg aag ccg gic gic gag 402

Asp Glu Ala Pro Leu Leu Ala Thr Tyr Ser Leu Lys Pro Val Val Glu

10

15

20

25

gcl tic gcc gcc acc gcg ggc atc gag gic gag acc cgc gat atc tcl 450

Ala Phe Ala Ala Thr Ala Gly Ile Glu Val Glu Thr Arg Asp Ile Ser

55

30

35

40

| | | |
|----|--|------|
| | ctc gcc ggt cgc atc ctc gca cag ttc gcg gac cag ctc ccc gag gag | 498 |
| | Leu Ala Gly Arg Ile Leu Ala Gln Phe Ala Asp Gln Leu Pro Glu Glu | |
| | 45 50 55 | |
| 5 | cag aag gtc tcc gac gcc ctc gcc gag ctc ggc gaa ctg gct aag acc | 546 |
| | Gln Lys Val Ser Asp Ala Leu Ala Glu Leu Gly Glu Leu Ala Lys Thr | |
| | 60 65 70 | |
| 10 | ccc gaa gcc aac atc atc aag ctt ccc aac atc tcc gca tcc gla ccg | 594 |
| | Pro Glu Ala Asn Ile Ile Lys Leu Pro Asn Ile Ser Ala Ser Val Pro | |
| | 75 80 85 | |
| 15 | cag ctc aag gct gcc gla aag gaa ctg cag gaa cag ggc tac gac ctg | 642 |
| | Gln Leu Lys Ala Ala Val Lys Glu Leu Gln Glu Gln Gly Tyr Asp Leu | |
| | 90 95 100 105 | |
| | ccc gag tac gag gat gcc aag gac cgc tac gcc gct gtc atc ggc tcc | 690 |
| | Pro Glu Tyr Glu Asp Ala Lys Asp Arg Tyr Ala Ala Val Ile Gly Ser | |
| 20 | 110 115 120 | |
| | aac gtc aac ccg gtc ctg cgc gag ggc aac tcc gac cgc cgc gca ccg | 738 |
| | Asn Val Asn Pro Val Leu Arg Glu Gly Asn Ser Asp Arg Arg Ala Pro | |
| | 125 130 135 | |
| 25 | gtg gcc gtg aag aac ttc gtg aag aag ttc ccc cac cgc atg ggc gag | 786 |
| | Val Ala Val Lys Asn Phe Val Lys Lys Phe Pro His Arg Met Gly Glu | |
| | 140 145 150 | |
| 30 | tggt tcc gcc gac tcc aag acc aac gtt gcc acc atg ggt gcc gac gac | 834 |
| | Trp Ser Ala Asp Ser Lys Thr Asn Val Ala Thr Met Gly Ala Asp Asp | |
| | 155 160 165 | |
| | ttc cgc agc aat gag aag tcc gtg atc atg gac gag gcc gac acc gtg | 882 |
| | Phe Arg Ser Asn Glu Lys Ser Val Ile Met Asp Glu Ala Asp Thr Val | |
| 35 | 170 175 180 185 | |
| | glg atc aag cat gtc gcc gcc gac ggc acc gag acc glg ctc aag gac | 930 |
| | Val Ile Lys His Val Ala Ala Asp Gly Thr Glu Thr Val Leu Lys Asp | |
| | 190 195 200 | |
| 40 | agc ctc ccc ctg ctc aag ggt gag gtc atc gac ggc acc ttc atc tcc | 978 |
| | Ser Leu Pro Leu Leu Lys Gly Glu Val Ile Asp Gly Thr Phe Ile Ser | |
| | 205 210 215 | |
| 45 | gcc aag gca ctg gac gcc ttc ctg ctc gac cag gtc aaa cgc gcc aag | 1026 |
| | Ala Lys Ala Leu Asp Ala Phe Leu Leu Asp Gln Val Lys Arg Ala Lys | |
| | 220 225 230 | |
| | gag gag ggc atc ctc ttc tcc gcc cac atg aag gcc acc atg atg aag | 1074 |
| | Glu Glu Gly Ile Leu Phe Ser Ala His Met Lys Ala Thr Met Met Lys | |
| 50 | 235 240 245 | |
| | glt tcc gac ccg atc atc ttc ggc cac atc gtc cgc gcc tac ttc gcc | 1122 |
| | Val Ser Asp Pro Ile Ile Phe Gly His Ile Val Arg Ala Tyr Phe Ala | |
| | 250 255 260 265 | |
| 55 | gat gtc tac gca cag tac ggt gag cag ctg ctc gcc gcc ggc ctc aac | 1170 |

| | Asp | Val | Tyr | Ala | Gln | Tyr | Gly | Glu | Gln | Leu | Leu | Ala | Ala | Gly | Leu | Asn | |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| | | | | | 270 | | | | 275 | | | | | | 280 | | |
| 5 | ggt | gag | aac | ggt | ctc | gcc | gcc | atc | tac | gcc | ggc | ctg | gac | aag | ctg | gac | 1218 |
| | Gly | Glu | Asn | Gly | Leu | Ala | Ala | Ile | Tyr | Ala | Gly | Leu | Asp | Lys | Leu | Asp | |
| | | | | 285 | | | | | 290 | | | | | 295 | | | |
| 10 | aac | ggt | gcc | gag | atc | aag | gca | gcc | ttc | gac | aag | ggc | ctg | gaa | gag | ggc | 1266 |
| | Asn | Gly | Ala | Glu | Ile | Lys | Ala | Ala | Phe | Asp | Lys | Gly | Leu | Glu | Glu | Gly | |
| | | | | 300 | | | | | 305 | | | | | 310 | | | |
| 15 | ccc | gac | ctg | gcc | atg | gig | aac | icc | gcc | aag | ggc | atc | acc | aac | ctg | cat | 1314 |
| | Pro | Asp | Leu | Ala | Met | Val | Asn | Ser | Ala | Lys | Gly | Ile | Thr | Asn | Leu | His | |
| | | | | 315 | | | | | 320 | | | | | 325 | | | |
| 20 | gtg | ccc | tcc | gat | gtc | atc | atc | gac | gcc | tcc | atg | ccc | gcc | atg | atc | cgc | 1362 |
| | Val | Pro | Ser | Asp | Val | Ile | Ile | Asp | Ala | Ser | Met | Pro | Ala | Met | Ile | Arg | |
| | | | | 330 | | | | | 335 | | | | | 340 | | 345 | |
| 25 | acc | icc | ggc | aag | atg | tgg | aac | aag | gac | gac | cag | acc | cag | gat | gcc | ctg | 1410 |
| | Thr | Ser | Gly | Lys | Met | Trp | Asn | Lys | Asp | Asp | Gln | Thr | Gln | Asp | Ala | Leu | |
| | | | | | 350 | | | | | 355 | | | | | 360 | | |
| 30 | gct | gtc | atc | ccg | gac | tcc | tcc | tac | gcc | ggt | gtc | tac | cag | acc | gtc | atc | 1458 |
| | Ala | Val | Ile | Pro | Asp | Ser | Ser | Tyr | Ala | Gly | Val | Tyr | Gln | Thr | Val | Ile | |
| | | | | 365 | | | | | 370 | | | | | 375 | | | |
| 35 | gag | gac | tgc | cgc | aag | aal | ggc | gcc | ttc | gat | ccg | acc | acc | atg | ggc | acc | 1506 |
| | Glu | Asp | Cys | Arg | Lys | Asn | Gly | Ala | Phe | Asp | Pro | Thr | Thr | Met | Gly | Thr | |
| | | | | 380 | | | | | 385 | | | | | 390 | | | |
| 40 | gtc | ccc | aac | gtc | ggt | ctg | atg | gca | cag | aag | gcc | gag | gag | tac | ggc | tcc | 1554 |
| | Val | Pro | Asn | Val | Gly | Leu | Met | Ala | Gln | Lys | Ala | Glu | Glu | Tyr | Gly | Ser | |
| | | | | 395 | | | | | 400 | | | | | 405 | | | |
| 45 | cac | gac | aag | acc | ttc | cgt | atc | gag | gcc | gac | ggc | aag | gta | cag | gtc | gtc | 1602 |
| | His | Asp | Lys | Thr | Phe | Arg | Ile | Glu | Ala | Asp | Gly | Lys | Val | Gln | Val | Val | |
| | | | | 410 | | | | | 415 | | | | | 420 | | 425 | |
| 50 | gcc | tcc | aac | ggt | gat | gtc | ctc | atc | gag | cac | gac | gtg | gag | aag | ggc | gac | 1650 |
| | Ala | Ser | Asn | Gly | Asp | Val | Leu | Ile | Glu | His | Asp | Val | Glu | Lys | Gly | Asp | |
| | | | | | 430 | | | | 435 | | | | | 440 | | | |
| 55 | atc | tgg | cgc | gcc | tgc | cag | acc | aag | gac | gcc | ccg | atc | cag | gac | tgg | gtc | 1698 |
| | Ile | Trp | Arg | Ala | Cys | Gln | Thr | Lys | Asp | Ala | Pro | Ile | Gln | Asp | Trp | Val | |
| | | | | 445 | | | | | 450 | | | | | 455 | | | |
| 60 | aag | ctg | gct | gtc | aac | cgc | gca | cgt | ctc | icc | ggc | atg | ccc | gct | gtg | ttc | 1746 |
| | Lys | Leu | Ala | Val | Asn | Arg | Ala | Arg | Leu | Ser | Gly | Met | Pro | Ala | Val | Phe | |
| | | | | 460 | | | | | 465 | | | | | 470 | | | |
| 65 | igg | ctg | gat | ccc | gcc | cgc | gca | cac | gac | cgc | aac | ctg | acc | aca | ctg | gtg | 1794 |
| | Trp | Leu | Asp | Pro | Ala | Arg | Ala | His | Asp | Arg | Asn | Leu | Thr | Thr | Leu | Val | |
| | | | | 475 | | | | | 480 | | | | | 485 | | | |
| 70 | gag | aag | tac | ctg | gca | gac | cac | gac | acc | gag | ggc | ctg | gac | atc | cag | atc | 1842 |
| | Glu | Lys | Tyr | Leu | Ala | Asp | His | Asp | Thr | Glu | Gly | Leu | Asp | Ile | Gln | Ile | |

| | | | | | | | | |
|----|---|---|------|--|-----|--|-----|--|
| | 490 | | 495 | | 500 | | 505 | |
| | ctc tcc ccc gtc | gag gcc acc cag cac gcc atc gac cgc atc cgc cgc | 1890 | | | | | |
| 5 | Leu Ser Pro Val | Glu Ala Thr Gln His Ala Ile Asp Arg Ile Arg Arg | | | | | | |
| | | 510 515 520 | | | | | | |
| | ggc gag gac acc atc tcc gtc acc ggt aac gtc ctg cgt gac tac aac | 1938 | | | | | | |
| | Gly Glu Asp Thr | Ile Ser Val Thr Gly Asn Val Leu Arg Asp Tyr Asn | | | | | | |
| 10 | | 525 530 535 | | | | | | |
| | acc gac ctc ttc ccg atc ctc gag ctg ggc acc tcc gcc aag atg ctc | 1986 | | | | | | |
| | Thr Asp Leu Phe | Pro Ile Leu Glu Leu Gly Thr Ser Ala Lys Met Leu | | | | | | |
| | | 540 545 550 | | | | | | |
| 15 | tcc gtc gtg cca ctg atg gcc ggc ggt gga ctc ttc gag acc ggt gcc | 2034 | | | | | | |
| | Ser Val Val Pro | Leu Met Ala Gly Gly Gly Leu Phe Glu Thr Gly Ala | | | | | | |
| | | 555 560 565 | | | | | | |
| | ggt ggc tcc gcc ccg aag cac gtc cag cag gtc atc gag gaa aac cac | 2082 | | | | | | |
| 20 | Gly Gly Ser Ala | Pro Lys His Val Gln Gln Val Ile Glu Glu Asn His | | | | | | |
| | | 570 575 580 585 | | | | | | |
| | ctg cgc tgg gat tcc ctc ggt gag ttc ctg gcc ctg gcc gag tcc ttc | 2130 | | | | | | |
| | Leu Arg Trp Asp | Ser Leu Gly Glu Phe Leu Ala Leu Ala Glu Ser Phe | | | | | | |
| 25 | | 590 595 600 | | | | | | |
| | cgc cac gag ctc aac acc cgc aac aac acc aag gcc ggt gtc ctc gcc | 2178 | | | | | | |
| | Arg His Glu Leu | Asn Thr Arg Asn Asn Thr Lys Ala Gly Val Leu Ala | | | | | | |
| | | 605 610 615 | | | | | | |
| 30 | gat gcc ctg gac cgt gcg acc gag aag ctc ctc aac gag gag aag tcc | 2226 | | | | | | |
| | Asp Ala Leu Asp | Arg Ala Thr Glu Lys Leu Leu Asn Glu Glu Lys Ser | | | | | | |
| | | 620 625 630 | | | | | | |
| | ccg tcc cgc aag gtc ggc gag atc gac aac cgt ggt tcc cac ttc tgg | 2274 | | | | | | |
| 35 | Pro Ser Arg Lys | Val Gly Glu Ile Asp Asn Arg Gly Ser His Phe Trp | | | | | | |
| | | 635 640 645 | | | | | | |
| | ctg gcc acc tac tgg gcc gat gaa ctg gcc aac cag acc gag gac gcc | 2322 | | | | | | |
| | Leu Ala Thr Tyr | Trp Ala Asp Glu Leu Ala Asn Gln Thr Glu Asp Ala | | | | | | |
| 40 | | 650 655 660 665 | | | | | | |
| | gag ctg gct gag acc ttc gcc cct gtc gcc gag gcc ctg aac aac cag | 2370 | | | | | | |
| | Glu Leu Ala Glu | Thr Phe Ala Pro Val Ala Glu Ala Leu Asn Asn Gln | | | | | | |
| | | 670 675 680 | | | | | | |
| 45 | gct gcc gac atc gac gca gca ctc atc ggt gag cag ggc aag cct gtc | 2418 | | | | | | |
| | Ala Ala Asp Ile | Asp Ala Ala Leu Ile Gly Glu Gln Gly Lys Pro Val | | | | | | |
| | | 685 690 695 | | | | | | |
| | gac ctg ggt ggc tac tac gca ccc tcc gat gag aag acc tcc gcg atc | 2466 | | | | | | |
| 50 | Asp Leu Gly Gly | Tyr Tyr Ala Pro Ser Asp Glu Lys Thr Ser Ala Ile | | | | | | |
| | | 700 705 710 | | | | | | |
| | atg cgc ccg glg gcc gca ttc aac gag atc atc gac tcc ctg aag aag | 2514 | | | | | | |
| 55 | Met Arg Pro Val | Ala Ala Phe Asn Glu Ile Ile Asp Ser Leu Lys Lys | | | | | | |
| | | 715 720 725 | | | | | | |

taaccccttc tccggagccg acagccgacg gccacgtcc cccgcccacg ggggaltcg 2574
 gccgtcgcc gttctggca clggaglgaa cacttcggig ataatggiga gaigaacagc 2634
 ccccgigtcc ccgccaicci gtccgccgtt tccgccggg gtclgalcgc tgcgtgggc 2694
 acccccgttg ccgtcgcaga caccalcacc gcggacacc accgggaaac clgcgtggcc 2754
 agccagaalg acaactccag cgtgalcagg ttcgggaltg acctggaggc cgaigtccgt 2814
 gagcagcgcc tgaccgaact ggalgcacag gaccccgcc tcaagaacga calcgaggcc 2874
 ttcatcgccg aggacccggt agccccctcc gcagccgalt tccagagacg gclggaltga 2934
 aatgacgccg gtgagggccl ggccatgcig claccigaat cccgcaccga ccccgagggt 2994
 gtggacctgc ag 3006

<210> 30

<211> 729

<212> PRT

<213> *Corynebacterium thermoaminogenes*

<400> 30

Met Ala Lys Ile Ile Trp Thr Arg Thr Asp Glu Ala Pro Leu Leu Ala

1 5 10 15

Thr Tyr Ser Leu Lys Pro Val Val Glu Ala Phe Ala Ala Thr Ala Gly

20 25 30

Ile Glu Val Glu Thr Arg Asp Ile Ser Leu Ala Gly Arg Ile Leu Ala

35 40 45

Gln Phe Ala Asp Gln Leu Pro Glu Glu Gln Lys Val Ser Asp Ala Leu

50 55 60

Ala Glu Leu Gly Glu Leu Ala Lys Thr Pro Glu Ala Asn Ile Ile Lys

65 70 75 80

Leu Pro Asn Ile Ser Ala Ser Val Pro Gln Leu Lys Ala Ala Val Lys

85 90 95

Glu Leu Gln Glu Gln Gly Tyr Asp Leu Pro Glu Tyr Glu Asp Ala Lys

100 105 110

Asp Arg Tyr Ala Ala Val Ile Gly Ser Asn Val Asn Pro Val Leu Arg

115 120 125

Glu Gly Asn Ser Asp Arg Arg Ala Pro Val Ala Val Lys Asn Phe Val

130 135 140

Lys Lys Phe Pro His Arg Met Gly Glu Trp Ser Ala Asp Ser Lys Thr

145 150 155 160

Asn Val Ala Thr Met Gly Ala Asp Asp Phe Arg Ser Asn Glu Lys Ser

165 170 175

Val Ile Met Asp Glu Ala Asp Thr Val Val Ile Lys His Val Ala Ala

180 185 190

Asp Gly Thr Glu Thr Val Leu Lys Asp Ser Leu Pro Leu Leu Lys Gly

195 200 205

Glu Val Ile Asp Gly Thr Phe Ile Ser Ala Lys Ala Leu Asp Ala Phe

| | | | | | | | | | | | | | | | | |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| | 210 | | 215 | | 220 | | | | | | | | | | | |
| | Leu | Leu | Asp | Gln | Val | Lys | Arg | Ala | Lys | Glu | Glu | Gly | Ile | Leu | Phe | Ser |
| | 225 | | | | | 230 | | | | | 235 | | | | | 240 |
| 5 | Ala | His | Met | Lys | Ala | Thr | Met | Met | Lys | Val | Ser | Asp | Pro | Ile | Ile | Phe |
| | | | | 245 | | | | | | | 250 | | | | | 255 |
| | Gly | His | Ile | Val | Arg | Ala | Tyr | Phe | Ala | Asp | Val | Tyr | Ala | Gln | Tyr | Gly |
| | | | 260 | | | | | | | 265 | | | | | 270 | |
| 10 | Glu | Gln | Leu | Leu | Ala | Ala | Gly | Leu | Asn | Gly | Glu | Asn | Gly | Leu | Ala | Ala |
| | | | 275 | | | | | | 280 | | | | | 285 | | |
| | Ile | Tyr | Ala | Gly | Leu | Asp | Lys | Leu | Asp | Asn | Gly | Ala | Glu | Ile | Lys | Ala |
| | 290 | | | | | | 295 | | | | | 300 | | | | |
| 15 | Ala | Phe | Asp | Lys | Gly | Leu | Glu | Glu | Gly | Pro | Asp | Leu | Ala | Met | Val | Asn |
| | 305 | | | | | 310 | | | | | 315 | | | | | 320 |
| | Ser | Ala | Lys | Gly | Ile | Thr | Asn | Leu | His | Val | Pro | Ser | Asp | Val | Ile | Ile |
| | | | | 325 | | | | | | | 330 | | | | | 335 |
| 20 | Asp | Ala | Ser | Met | Pro | Ala | Met | Ile | Arg | Thr | Ser | Gly | Lys | Met | Trp | Asn |
| | | | | 340 | | | | | | 345 | | | | | 350 | |
| | Lys | Asp | Asp | Gln | Thr | Gln | Asp | Ala | Leu | Ala | Val | Ile | Pro | Asp | Ser | Ser |
| | | 355 | | | | | | 360 | | | | | 365 | | | |
| 25 | Tyr | Ala | Gly | Val | Tyr | Gln | Thr | Val | Ile | Glu | Asp | Cys | Arg | Lys | Asn | Gly |
| | 370 | | | | | | 375 | | | | 380 | | | | | |
| | Ala | Phe | Asp | Pro | Thr | Thr | Met | Gly | Thr | Val | Pro | Asn | Val | Gly | Leu | Met |
| 30 | 385 | | | | | 390 | | | | | 395 | | | | | 400 |
| | Ala | Gln | Lys | Ala | Glu | Glu | Tyr | Gly | Ser | His | Asp | Lys | Thr | Phe | Arg | Ile |
| | | | | 405 | | | | | | 410 | | | | | 415 | |
| | Glu | Ala | Asp | Gly | Lys | Val | Gln | Val | Val | Ala | Ser | Asn | Gly | Asp | Val | Leu |
| 35 | | | 420 | | | | | | 425 | | | | | 430 | | |
| | Ile | Glu | His | Asp | Val | Glu | Lys | Gly | Asp | Ile | Trp | Arg | Ala | Cys | Gln | Thr |
| | | 435 | | | | | | 440 | | | | 445 | | | | |
| | Lys | Asp | Ala | Pro | Ile | Gln | Asp | Trp | Val | Lys | Leu | Ala | Val | Asn | Arg | Ala |
| 40 | | 450 | | | | | 455 | | | | | 460 | | | | |
| | Arg | Leu | Ser | Gly | Met | Pro | Ala | Val | Phe | Trp | Leu | Asp | Pro | Ala | Arg | Ala |
| | 465 | | | | | 470 | | | | | 475 | | | | | 480 |
| | His | Asp | Arg | Asn | Leu | Thr | Thr | Leu | Val | Glu | Lys | Tyr | Leu | Ala | Asp | His |
| 45 | | | | 485 | | | | | | 490 | | | | | 495 | |
| | Asp | Thr | Glu | Gly | Leu | Asp | Ile | Gln | Ile | Leu | Ser | Pro | Val | Glu | Ala | Thr |
| | | 500 | | | | | | | 505 | | | | | 510 | | |
| | Gln | His | Ala | Ile | Asp | Arg | Ile | Arg | Arg | Gly | Glu | Asp | Thr | Ile | Ser | Val |
| 50 | | 515 | | | | | | 520 | | | | | 525 | | | |
| | Thr | Gly | Asn | Val | Leu | Arg | Asp | Tyr | Asn | Thr | Asp | Leu | Phe | Pro | Ile | Leu |
| | | 530 | | | | | 535 | | | | | 540 | | | | |
| | Glu | Leu | Gly | Thr | Ser | Ala | Lys | Met | Leu | Ser | Val | Pro | Leu | Met | Ala | |
| 55 | 545 | | | | | 550 | | | | | 555 | | | | 560 | |

Gly Gly Gly Leu Phe Glu Thr Gly Ala Gly Gly Ser Ala Pro Lys His

565

570

575

Val Gln Gln Val Ile Glu Glu Asn His Leu Arg Trp Asp Ser Leu Gly

580

585

590

Glu Phe Leu Ala Leu Ala Glu Ser Phe Arg His Glu Leu Asn Thr Arg

595

600

605

Asn Asn Thr Lys Ala Gly Val Leu Ala Asp Ala Leu Asp Arg Ala Thr

610

615

620

Glu Lys Leu Leu Asn Glu Glu Lys Ser Pro Ser Arg Lys Val Gly Glu

625

630

635

640

Ile Asp Asn Arg Gly Ser His Phe Trp Leu Ala Thr Tyr Trp Ala Asp

645

650

655

Glu Leu Ala Asn Gln Thr Glu Asp Ala Glu Leu Ala Glu Thr Phe Ala

660

665

670

Pro Val Ala Glu Ala Leu Asn Asn Gln Ala Ala Asp Ile Asp Ala Ala

675

680

685

Leu Ile Gly Glu Gln Gly Lys Pro Val Asp Leu Gly Gly Tyr Tyr Ala

690

695

700

Pro Ser Asp Glu Lys Thr Ser Ala Ile Met Arg Pro Val Ala Ala Phe

705

710

715

720

Asn Glu Ile Ile Asp Ser Leu Lys Lys

725

<210> 31

<211> 2322

<212> DNA

<213> *Corynebacterium thermoaminogenes*

<220>

<221> CDS

<222> (806)..(2212)

<400> 31

ggtaccccca cgtaccctag gccatcacag caatttttac atcggaatatt ttaggigtgc 60

tcataacgtc cttatgaatt tgcagttat tagttattta aatagagaat caaacaccga 120

ccitagccctc gccgaigcta aaagtcagct gaccccttgg ggcgcttcat ttgaaactgc 180

gaccaagctc atgaatgcgc gaaagcattt ccattataag ggtaagcigt aagaatagtg 240

ggagaaaaatg ttcagtcgtg ttctaactca cttagagaaat tccatttttc tgggccttc 300

tcaaalagat taagttggccc gtaigcttga ttcttagaat atttagaagc gcgccaactc 360

atgattatgt attgtataag cctcaaagac cgaalagatt actaacattt aagttggacca 420

gagcgltaga agctttttag agtgcctcatt ccttgcctgac ggcaagggtt tcttaccatg 480

agatagatcg gcagatagtt gglttgtaaa aatttttlaag gacggctcgc aatgtcaatt 540

cttgaacaga tcatcttctt catcaacacc atcttgggtt atggctctga cgtctgttct 600

tccgcctcca gcaacccttc tcacacgac gccctgctt aggcctaatt gglaataagg 660
 ctgiglaaca gtcgcccgcg tgattgtgc tttttaggcg cccgcgcggg cgatttcgg 720
 5 ttttcalctt ttttlaaatig agtttggaag atcaagtgcc cccggatgca cgacaatgct 780
 atgccgaaca cgtattgtig aaatc gtg act gaa cat tat gac gta gla gta 832
 Val Thr Glu His Tyr Asp Val Val Val
 1 5
 10 ctc gga gct ggc ccc ggt ggc tat gtc tcc gcc atc cgc gcc gcg cag 880
 Leu Gly Ala Gly Pro Gly Gly Tyr Val Ser Ala Ile Arg Ala Ala Gln
 10 15 20 25
 ctc ggt aag aaa gtt ggc gtt atc gag aag cag tac tgg gga ggt gtc 928
 15 Leu Gly Lys Lys Val Ala Val Ile Glu Lys Gln Tyr Trp Gly Gly Val
 30 35 40
 tgc ctg aat gtg ggt tgt atc cca tct aag gcg ttg atc aag aac gct 976
 Cys Leu Asn Val Gly Cys Ile Pro Ser Lys Ala Leu Ile Lys Asn Ala
 45 50 55
 20 gag atc gcc cac atc ttc aac cat gag aag aag acc ttc ggc atc aac 1024
 Glu Ile Ala His Ile Phe Asn His Glu Lys Lys Thr Phe Gly Ile Asn
 60 65 70
 25 ggc gag gtc acc ttc aac tac gag gat gcc cac aag cgt tcc cgt ggt 1072
 Gly Glu Val Thr Phe Asn Tyr Glu Asp Ala His Lys Arg Ser Arg Gly
 75 80 85
 gtc tcc gac aag atc gtc ggc ggt gtt cac tac ttg atg aag aag aac 1120
 30 Val Ser Asp Lys Ile Val Gly Gly Val His Tyr Leu Met Lys Lys Asn
 90 95 100 105
 aag atc acc gag atc gac ggt ttc ggc acc ttc aag gat gcc aag acc 1168
 Lys Ile Thr Glu Ile Asp Gly Phe Gly Thr Phe Lys Asp Ala Lys Thr
 110 115 120
 35 atc gag gtg acc gat ggt aag gat gcc ggc aag acc gtc acc ttc gat 1216
 Ile Glu Val Thr Asp Gly Lys Asp Ala Gly Lys Thr Val Thr Phe Asp
 125 130 135
 40 gac tgc atc atc gcc acc ggt tcc gtg gtc aac tcc ctc cgt ggt gtt 1264
 Asp Cys Ile Ile Ala Thr Gly Ser Val Val Asn Ser Leu Arg Gly Val
 140 145 150
 gag ttc tcc gag aac gtg gtc tcc tac gag gag cag atc ctc aac ccg 1312
 45 Glu Phe Ser Glu Asn Val Val Ser Tyr Glu Glu Gln Ile Leu Asn Pro
 155 160 165
 gtg gcg cct aag aag atg gtc atc gtc ggt ggc ggc gcc atc ggt atg 1360
 Val Ala Pro Lys Lys Met Val Ile Val Gly Gly Gly Ala Ile Gly Met
 170 175 180 185
 50 gaa ttc gcc tac gtt ctg ggc aac tac ggt gtg gac gla acc ctc atc 1408
 Glu Phe Ala Tyr Val Leu Gly Asn Tyr Gly Val Asp Val Thr Leu Ile
 190 195 200
 55 gag ttc atg gac cgc gtt ctg ccg aac gag gat cca gag gtg tcc aag 1456

EP 1 219 712 A1

| | Glu | Phe | Met | Asp | Arg | Val | Leu | Pro | Asn | Glu | Asp | Pro | Glu | Val | Ser | Lys | |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| | | | | 205 | | | | | 210 | | | | | 215 | | | |
| 5 | gtt | atc | gcc | aag | gcc | tac | aag | aag | atg | ggc | atc | aag | cic | cic | ccg | ggc | 1504 |
| | Val | Ile | Ala | Lys | Ala | Tyr | Lys | Lys | Met | Gly | Ile | Lys | Leu | Leu | Pro | Gly | |
| | | | 220 | | | | | 225 | | | | | 230 | | | | |
| 10 | cac | gca | acc | acc | gcg | gig | cgc | gac | aal | ggc | gat | icc | glt | gag | gic | gat | 1552 |
| | His | Ala | Thr | Thr | Ala | Val | Arg | Asp | Asn | Gly | Asp | Ser | Val | Glu | Val | Asp | |
| | | | 235 | | | | 240 | | | | | 245 | | | | | |
| 15 | tac | cag | aag | aag | ggc | icg | gac | aag | acc | gag | acc | atc | acc | gic | gac | cgt | 1600 |
| | Tyr | Gln | Lys | Lys | Gly | Ser | Asp | Lys | Thr | Glu | Thr | Ile | Thr | Val | Asp | Arg | |
| | 250 | | | | | 255 | | | | 260 | | | | | 265 | | |
| 20 | gtt | ctt | atc | icc | gic | ggc | ttc | cgc | cca | cgc | gic | gag | ggc | ttc | ggc | cig | 1648 |
| | Val | Leu | Ile | Ser | Val | Gly | Phe | Arg | Pro | Arg | Val | Glu | Gly | Phe | Gly | Leu | |
| | | | | 270 | | | | 275 | | | | 280 | | | | | |
| 25 | gag | aac | acc | ggc | gic | aag | cic | acc | gaa | cgc | ggt | gcc | atc | gac | att | gat | 1696 |
| | Glu | Asn | Thr | Gly | Val | Lys | Leu | Thr | Glu | Arg | Gly | Ala | Ile | Asp | Ile | Asp | |
| | | | 285 | | | | | 290 | | | | 295 | | | | | |
| 30 | gag | cat | atg | cgc | acc | aac | gic | gac | ggc | atc | tac | gcc | atc | ggt | gac | gic | 1744 |
| | Glu | His | Met | Arg | Thr | Asn | Val | Asp | Gly | Ile | Tyr | Ala | Ile | Gly | Asp | Val | |
| | | | 300 | | | | 305 | | | | | 310 | | | | | |
| 35 | acc | gcc | aag | cig | cag | cig | gca | cac | gic | gcc | gag | gca | cag | ggc | att | gic | 1792 |
| | Thr | Ala | Lys | Leu | Gln | Leu | Ala | His | Val | Ala | Glu | Ala | Gln | Gly | Ile | Val | |
| | | | 315 | | | 320 | | | | | 325 | | | | | | |
| 40 | gcc | gcc | gag | aca | cic | gcc | ggc | gca | gaa | acc | cag | acc | cig | ggc | gac | tac | 1840 |
| | Ala | Ala | Glu | Thr | Leu | Ala | Gly | Ala | Glu | Thr | Gln | Thr | Leu | Gly | Asp | Tyr | |
| | 330 | | | 335 | | | | 340 | | | | 345 | | | | | |
| 45 | atg | atg | atg | ccg | cgt | gcc | acc | ttc | tgc | aac | cca | cag | glt | gcc | tcc | ttc | 1888 |
| | Met | Met | Met | Pro | Arg | Ala | Thr | Phe | Cys | Asn | Pro | Gln | Val | Ala | Ser | Phe | |
| | | | 350 | | | | 355 | | | | | 360 | | | | | |
| 50 | ggt | tac | acc | gag | gag | cag | gcc | aag | gag | aag | tgg | ccg | gat | cga | gag | atc | 1936 |
| | Gly | Tyr | Thr | Glu | Glu | Gln | Ala | Lys | Glu | Lys | Trp | Pro | Asp | Arg | Glu | Ile | |
| | | | 365 | | | | 370 | | | | | 375 | | | | | |
| 55 | aag | gig | tcc | tcc | ttc | ccg | ttc | tcc | gcg | aac | ggc | aag | gcc | gic | ggc | cig | 1984 |
| | Lys | Val | Ser | Ser | Phe | Pro | Phe | Ser | Ala | Asn | Gly | Lys | Ala | Val | Gly | Leu | |
| | | | 380 | | | | 385 | | | | | 390 | | | | | |
| 60 | gct | gag | acc | gat | ggt | ttc | gcc | aag | atc | gic | gcc | gac | gct | gag | ttc | ggt | 2032 |
| | Ala | Glu | Thr | Asp | Gly | Phe | Ala | Lys | Ile | Val | Ala | Asp | Ala | Glu | Phe | Gly | |
| | | | 395 | | | 400 | | | | | 405 | | | | | | |
| 65 | gaa | cig | cig | ggt | ggc | cac | att | gic | ggt | gcc | aac | gcc | tcc | gag | cig | cic | 2080 |
| | Glu | Leu | Leu | Gly | Gly | His | Ile | Val | Gly | Ala | Asn | Ala | Ser | Glu | Leu | Leu | |
| | 410 | | | 415 | | | 420 | | | | 425 | | | | | | |
| 70 | aac | gag | cig | gig | cig | gcc | cag | aac | tgg | gat | cic | acc | acc | gag | gag | atc | 2128 |
| | Asn | Glu | Leu | Val | Leu | Ala | Gln | Asn | Trp | Asp | Leu | Thr | Thr | Glu | Glu | Ile | |

430 435 440
 agc cgc agc gtc cac atc cac ccg acc ctc tgc gag gct gtc aag gaa 2176
 Ser Arg Ser Val His Ile His Pro Thr Leu Ser Glu Ala Val Lys Glu
 5 445 450 455
 gct gcc cac ggc gtc aac ggc cac atg atc aac ttc taaatcccgt 2222
 Ala Ala His Gly Val Asn Gly His Met Ile Asn Phe
 10 460 465
 cagacaaatg caaatccct caccgaiggc atalcggiga ggggatitc tcatgcacgt 2282
 aaaatcataa tccatggcaa ggaaagtcga caacagcgcc 2322
 15 <210> 32
 <211> 469
 <212> PRT
 <213> Corynebacterium thermoaminogenes
 20 <400> 32
 Val Thr Glu His Tyr Asp Val Val Val Leu Gly Ala Gly Pro Gly Gly
 1 5 10 15
 Tyr Val Ser Ala Ile Arg Ala Ala Gln Leu Gly Lys Lys Val Ala Val
 25 20 25 30
 Ile Glu Lys Gln Tyr Trp Gly Gly Val Cys Leu Asn Val Gly Cys Ile
 35 40 45
 Pro Ser Lys Ala Leu Ile Lys Asn Ala Glu Ile Ala His Ile Phe Asn
 50 55 60
 His Glu Lys Lys Thr Phe Gly Ile Asn Gly Glu Val Thr Phe Asn Tyr
 65 70 75 80
 Glu Asp Ala His Lys Arg Ser Arg Gly Val Ser Asp Lys Ile Val Gly
 35 85 90 95
 Gly Val His Tyr Leu Met Lys Lys Asn Lys Ile Thr Glu Ile Asp Gly
 100 105 110
 Phe Gly Thr Phe Lys Asp Ala Lys Thr Ile Glu Val Thr Asp Gly Lys
 40 115 120 125
 Asp Ala Gly Lys Thr Val Thr Phe Asp Asp Cys Ile Ile Ala Thr Gly
 130 135 140
 Ser Val Val Asn Ser Leu Arg Gly Val Glu Phe Ser Glu Asn Val Val
 45 145 150 155 160
 Ser Tyr Glu Glu Gln Ile Leu Asn Pro Val Ala Pro Lys Lys Met Val
 165 170 175
 Ile Val Gly Gly Gly Ala Ile Gly Met Glu Phe Ala Tyr Val Leu Gly
 50 180 185 190
 Asn Tyr Gly Val Asp Val Thr Leu Ile Glu Phe Met Asp Arg Val Leu
 195 200 205
 55 Pro Asn Glu Asp Pro Glu Val Ser Lys Val Ile Ala Lys Ala Tyr Lys

| | 210 | 215 | 220 |
|----|---|---|-------------|
| | Lys Met Gly Ile | Lys Leu Leu Pro Gly His Ala Thr Thr Ala Val Arg | |
| 5 | 225 | 230 | 235 240 |
| | Asp Asn Gly Asp Ser Val Glu Val Asp Tyr Gln Lys Lys Gly Ser Asp | | |
| | | 245 | 250 255 |
| | Lys Thr Glu Thr Ile Thr Val Asp Arg Val Leu Ile Ser Val Gly Phe | | |
| 10 | | 260 | 265 270 |
| | Arg Pro Arg Val Glu Gly Phe Gly Leu Glu Asn Thr Gly Val Lys Leu | | |
| | | 275 | 280 285 |
| | Thr Glu Arg Gly Ala Ile Asp Ile Asp Glu His Met Arg Thr Asn Val | | |
| 15 | | 290 | 295 300 |
| | Asp Gly Ile Tyr Ala Ile Gly Asp Val Thr Ala Lys Leu Gln Leu Ala | | |
| | 305 | 310 | 315 320 |
| | His Val Ala Glu Ala Gln Gly Ile Val Ala Ala Glu Thr Leu Ala Gly | | |
| 20 | | 325 | 330 335 |
| | Ala Glu Thr Gln Thr Leu Gly Asp Tyr Met Met Met Pro Arg Ala Thr | | |
| | | 340 | 345 350 |
| | Phe Cys Asn Pro Gln Val Ala Ser Phe Gly Tyr Thr Glu Glu Gln Ala | | |
| 25 | | 355 | 360 365 |
| | Lys Glu Lys Trp Pro Asp Arg Glu Ile Lys Val Ser Ser Phe Pro Phe | | |
| | | 370 | 375 380 |
| | Ser Ala Asn Gly Lys Ala Val Gly Leu Ala Glu Thr Asp Gly Phe Ala | | |
| 30 | | 385 | 390 395 400 |
| | Lys Ile Val Ala Asp Ala Glu Phe Gly Glu Leu Leu Gly Gly His Ile | | |
| | | 405 | 410 415 |
| | Val Gly Ala Asn Ala Ser Glu Leu Leu Asn Glu Leu Val Leu Ala Gln | | |
| 35 | | 420 | 425 430 |
| | Asn Trp Asp Leu Thr Thr Glu Glu Ile Ser Arg Ser Val His Ile His | | |
| | | 435 | 440 445 |
| | Pro Thr Leu Ser Glu Ala Val Lys Glu Ala Ala His Gly Val Asn Gly | | |
| 40 | | 450 | 455 460 |
| | His Met Ile Asn Phe | | |
| | 465 | | |

<210> 33

<211> 4096

<212> DNA

<213> Corynebacterium thermoaminogenes

<220>

<221> CDS

<222> (250)...(3951)

<400> 33

ccggaicac gtgggtgacg ggggacgtat catcgaggat ggltcccacg atgaacttct 60
 5 gggagcgaat ggaacctacg caacaatgtg gcatttagta gggtagacagg atatttagg 120
 aaagacttgt taccaaaagg tgctaatact ggggtgctag gtccccgga ccggaaccag 180
 cgttacagtg gataaaaataa agcccatlta gaaccttcaa caagcaagga aaagaggcga 240
 gtacctgcc gtg agc agc gct agt act ttc ggc cag aac gcg tgg ctg gtg 291
 Val Ser Ser Ala Ser Thr Phe Gly Gln Asn Ala Trp Leu Val
 10 1 5 10
 gat gag atg ttc cag cag ttc aag aag gac ccc cag tcc gtg gac aag 339
 Asp Glu Met Phe Gln Gln Phe Lys Lys Asp Pro Gln Ser Val Asp Lys
 15 15 20 25 30
 gaa tgg aga gag ctg ttc gag tct cag ggg ggt ccc cag gct gaa aag 387
 Glu Trp Arg Glu Leu Phe Glu Ser Gln Gly Gly Pro Gln Ala Glu Lys
 35 35 40 45
 gct acc ccc gcc acc ccc gaa gcc aag aag gca gct tgg tgg cag tcc 435
 Ala Thr Pro Ala Thr Pro Glu Ala Lys Lys Ala Ala Ser Ser Gln Ser
 50 50 55 60
 tca act tcc gga cag tcc acc gcc aag gct gcc cct gcc gcc aag acc 483
 25 Ser Thr Ser Gly Gln Ser Thr Ala Lys Ala Ala Pro Ala Ala Lys Thr
 65 70 75
 gca cgg gcc tct gcg cca gcc aag gct gcc cct gtt aag caa aac cag 531
 Ala Pro Ala Ser Ala Pro Ala Lys Ala Ala Pro Val Lys Gln Asn Gln
 80 85 90
 gcg tcc aag cct gcc aag aag gcc aag gag tcc ccc ctg tcc aag cca 579
 Ala Ser Lys Pro Ala Lys Lys Ala Lys Glu Ser Pro Leu Ser Lys Pro
 95 100 105 110
 gct gcc atg cct gag ccg gga acc acc cca ctg agg ggc atc ttc aag 627
 Ala Ala Met Pro Glu Pro Gly Thr Thr Pro Leu Arg Gly Ile Phe Lys
 115 120 125
 tcc atc gcc aag aac atg gac ctg tcc ctg gag gtg ccc acc gcc acc 675
 40 Ser Ile Ala Lys Asn Met Asp Leu Ser Leu Glu Val Pro Thr Ala Thr
 130 135 140
 tcc gtc cgc gac atg ccc gcg cgc ctg atg ttc gag aac cgc gcc atg 723
 45 Ser Val Arg Asp Met Pro Ala Arg Leu Met Phe Glu Asn Arg Ala Met
 145 150 155
 gtc aac gac cag ctg aag cgc acc cgt ggc ggc aag atc tcc ttc acc 771
 Val Asn Asp Gln Leu Lys Arg Thr Arg Gly Gly Lys Ile Ser Phe Thr
 160 165 170
 cac atc atc ggc tac gcc atg gtg aag gct gtc atg gca cac ccg gac 819
 His Ile Ile Gly Tyr Ala Met Val Lys Ala Val Met Ala His Pro Asp
 175 180 185 190
 atg aac aac tcc tat gac atc gtc gac ggc aag ccg tcc ctg gtc gtc 867
 55 Met Asn Asn Ser Tyr Asp Ile Val Asp Gly Lys Pro Ser Leu Val Val

| | 195 | 200 | 205 | |
|----|---|------|-----|--|
| | ccg gag cac atc aac ctc ggc ctg gcc atc gac ctc ccc cag aag gac | 915 | | |
| 5 | Pro Glu His Ile Asn Leu Gly Leu Ala Ile Asp Leu Pro Gln Lys Asp | | | |
| | 210 215 220 | | | |
| | ggc tcc cgt gcc ctc gtc gtc gcc gcc atc aag gaa acc gag aag atg | 963 | | |
| | Gly Ser Arg Ala Leu Val Val Ala Ala Ile Lys Glu Thr Glu Lys Met | | | |
| 10 | 225 230 235 | | | |
| | acc ttc tcc cag ttc ctg gag gcc tat gag gac gtt gtc gca cgc tcc | 1011 | | |
| | Thr Phe Ser Gln Phe Leu Glu Ala Tyr Glu Asp Val Val Ala Arg Ser | | | |
| | 240 245 250 | | | |
| 15 | cgc gtc ggc aag ctc acc atg gat gac tac cag ggt gtc acc atc tcc | 1059 | | |
| | Arg Val Gly Lys Leu Thr Met Asp Asp Tyr Gln Gly Val Thr Ile Ser | | | |
| | 255 260 265 270 | | | |
| | tig acc aac ccg ggt gcc atc ggt acc cgc cac tcc atc ccg cgt ctg | 1107 | | |
| 20 | Leu Thr Asn Pro Gly Gly Ile Gly Thr Arg His Ser Ile Pro Arg Leu | | | |
| | 275 280 285 | | | |
| | acc aag ggc cag gcc acc atc atc ggt gtc ggt tcc atg gac tac ccg | 1155 | | |
| | Thr Lys Gly Gln Gly Thr Ile Ile Gly Val Gly Ser Met Asp Tyr Pro | | | |
| 25 | 290 295 300 | | | |
| | gcc gag ttc cag ggt gcc tcc gag gac cgt ctc gcc gag ctc ggt gtc | 1203 | | |
| | Ala Glu Phe Gln Gly Ala Ser Glu Asp Arg Leu Ala Glu Leu Gly Val | | | |
| | 305 310 315 | | | |
| 30 | ggc aag ctc gtc acc atc acc tcc acc tac gat cac cgc gtc atc cag | 1251 | | |
| | Gly Lys Leu Val Thr Ile Thr Ser Thr Tyr Asp His Arg Val Ile Gln | | | |
| | 320 325 330 | | | |
| | ggc gcg gaa tcc ggt gag ttc ctg cgc acc atg tcc cag ctg ctc gtc | 1299 | | |
| 35 | Gly Ala Glu Ser Gly Glu Phe Leu Arg Thr Met Ser Gln Leu Leu Val | | | |
| | 335 340 345 350 | | | |
| | gac gat gcg ttc tgg gat cac atc ttc gag gag atg aac gtt ccc tac | 1347 | | |
| | Asp Asp Ala Phe Trp Asp His Ile Phe Glu Glu Met Asn Val Pro Tyr | | | |
| 40 | 355 360 365 | | | |
| | acc ccg atg cgc tgg gca cag gac ctg ccc aac acc ggt gtc gac aag | 1395 | | |
| | Thr Pro Met Arg Trp Ala Gln Asp Leu Pro Asn Thr Gly Val Asp Lys | | | |
| | 370 375 380 | | | |
| 45 | aac acc cgt gtc atg cag ctc atc gag gcc tac cgc tcc cgc ggt cac | 1443 | | |
| | Asn Thr Arg Val Met Gln Leu Ile Glu Ala Tyr Arg Ser Arg Gly His | | | |
| | 385 390 395 | | | |
| | ctc atc gcc gac acc aac cca ctg ccc tgg gtc cag ccc ggc atg ccc | 1491 | | |
| 50 | Leu Ile Ala Asp Thr Asn Pro Leu Pro Trp Val Gln Pro Gly Met Pro | | | |
| | 400 405 410 | | | |
| | gtc ccg gat cac cgt gac ctc gac atc gag acc cac ggc ctg acc ctg | 1539 | | |
| | Val Pro Asp His Arg Asp Leu Asp Ile Glu Thr His Gly Leu Thr Leu | | | |
| 55 | 415 420 425 430 | | | |

| | | |
|----|---|------|
| | 1gg gat ctg gac cgt acc ttc cac gtc ggt ggt ttc ggt ggc aag gag | 1587 |
| | Trp Asp Leu Asp Arg Thr Phe His Val Gly Gly Phe Gly Gly Lys Glu | |
| 5 | 435 440 445 | |
| | acc atg acc ctg cgc gag glg ctc agc cgc ctc cgc gcc gcc tac acc | 1635 |
| | Thr Met Thr Leu Arg Glu Val Leu Ser Arg Leu Arg Ala Ala Tyr Thr | |
| | 450 455 460 | |
| 10 | ctc aag gtc ggc tcc gag tac acc cac atc ctc gac cgc gat gag cgc | 1683 |
| | Leu Lys Val Gly Ser Glu Tyr Thr His Ile Leu Asp Arg Asp Glu Arg | |
| | 465 470 475 | |
| | acc tgg ctg cag gac cgc ctc gag gcc ggt atg ccc aag ccc acc gcc | 1731 |
| 15 | Thr Trp Leu Gln Asp Arg Leu Glu Ala Gly Met Pro Lys Pro Thr Ala | |
| | 480 485 490 | |
| | gcc gag cag aag tac atc ctg cag aag ctc aac gcc gcc gag gca ttc | 1779 |
| | Ala Glu Gln Lys Tyr Ile Leu Gln Lys Leu Asn Ala Ala Glu Ala Phe | |
| 20 | 495 500 505 510 | |
| | gag aac ttc ctg cag acc aag tac gtc ggc cag aag cgt ttc tcc ctc | 1827 |
| | Glu Asn Phe Leu Gln Thr Lys Tyr Val Gly Gln Lys Arg Phe Ser Leu | |
| | 515 520 525 | |
| 25 | gag ggt gcc gag tca ctg atc ccg ctg atg gac tcc gcc atc gac acc | 1875 |
| | Glu Gly Ala Glu Ser Leu Ile Pro Leu Met Asp Ser Ala Ile Asp Thr | |
| | 530 535 540 | |
| | gcc gca ggc cag ggc ctt gac gag gtc gtc atc ggc atg ccc cac cgt | 1923 |
| 30 | Ala Ala Gly Gln Gly Leu Asp Glu Val Val Ile Gly Met Pro His Arg | |
| | 545 550 555 | |
| | ggt cgc ctc aac glg ctg ttc aac atc gtc ggc aag cca ctg gcc tcc | 1971 |
| | Gly Arg Leu Asn Val Leu Phe Asn Ile Val Gly Lys Pro Leu Ala Ser | |
| 35 | 560 565 570 | |
| | atc ttc aac gag ttc gag ggc cag atg gag cag ggc cag atc ggt ggc | 2019 |
| | Ile Phe Asn Glu Phe Glu Gly Gln Met Glu Gln Gly Gln Ile Gly Gly | |
| | 575 580 585 590 | |
| 40 | tcc ggt gac glg aag tac cac ctc ggt tcc gag ggc acc cac ctg cag | 2067 |
| | Ser Gly Asp Val Lys Tyr His Leu Gly Ser Glu Gly Thr His Leu Gln | |
| | 595 600 605 | |
| | atg ttc ggc gac ggc gag atc aag gtc tcc ctc acc gcc aac ccc tcc | 2115 |
| 45 | Met Phe Gly Asp Gly Glu Ile Lys Val Ser Leu Thr Ala Asn Pro Ser | |
| | 610 615 620 | |
| | cac ctc gag gcc gtc aac ccg gtc glg gag ggc atc gtc cgc gcc aag | 2163 |
| | His Leu Glu Ala Val Asn Pro Val Val Glu Gly Ile Val Arg Ala Lys | |
| 50 | 625 630 635 | |
| | cag gac atc ctg gac aag ggc ccg gac ggc tac acc gtc gtc ccg ctg | 2211 |
| | Gln Asp Ile Leu Asp Lys Gly Pro Asp Gly Tyr Thr Val Val Pro Leu | |
| | 640 645 650 | |
| 55 | ctg ctc cac ggt gac gcc gcc ttc gcc ggc ctg ggc atc glg ccc gag | 2259 |

| | | | | | | | | | | | | | | | | | |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| | Leu | Leu | His | Gly | Asp | Ala | Ala | Phe | Ala | Gly | Leu | Gly | Ile | Val | Pro | Glu | |
| | 655 | | | | | 660 | | | | | 665 | | | | | 670 | |
| 5 | acc | atc | aac | ctc | gca | gcc | ctg | cgt | ggt | tac | gat | gtc | ggt | ggc | acc | atc | 2307 |
| | Thr | Ile | Asn | Leu | Ala | Ala | Leu | Arg | Gly | Tyr | Asp | Val | Gly | Gly | Thr | Ile | |
| | | | | | 675 | | | | | 680 | | | | | 685 | | |
| 10 | cac | atc | gtg | gtc | aac | aac | cag | atc | ggc | ttc | acc | acc | acc | ccg | gac | icc | 2355 |
| | His | Ile | Val | Val | Asn | Asn | Gln | Ile | Gly | Phe | Thr | Thr | Thr | Pro | Asp | Ser | |
| | | | | | 690 | | | | | 695 | | | | | 700 | | |
| | agc | cgt | tcc | atg | cac | tac | gcc | acc | gac | tgc | gcc | aag | gcc | ttc | ggt | tgc | 2403 |
| | Ser | Arg | Ser | Met | His | Tyr | Ala | Thr | Asp | Cys | Ala | Lys | Ala | Phe | Gly | Cys | |
| 15 | | | 705 | | | | | 710 | | | | | 715 | | | | |
| | ccg | gtg | ttc | cac | gic | aac | ggt | gac | gac | ccc | gag | gct | glg | gic | igg | gic | 2451 |
| | Pro | Val | Phe | His | Val | Asn | Gly | Asp | Asp | Pro | Glu | Ala | Val | Val | Trp | Val | |
| | | | 720 | | | | 725 | | | | | 730 | | | | | |
| 20 | ggc | cag | ctg | gcc | acc | gag | tac | cgt | cgc | cgc | ttc | ggc | aag | gat | gtc | ttc | 2499 |
| | Gly | Gln | Leu | Ala | Thr | Glu | Tyr | Arg | Arg | Arg | Phe | Gly | Lys | Asp | Val | Phe | |
| | 735 | | | | | 740 | | | | | 745 | | | | 750 | | |
| | atc | gac | ctc | atc | tgc | tac | cgc | ctg | cgc | ggc | cac | aac | gag | gct | gat | gac | 2547 |
| 25 | Ile | Asp | Leu | Ile | Cys | Tyr | Arg | Leu | Arg | Gly | His | Asn | Glu | Ala | Asp | Asp | |
| | | | | | 755 | | | | | 760 | | | | | 765 | | |
| | cca | tcc | atg | acc | cag | ccg | aag | atg | tac | gag | ctg | atc | acc | ggc | cgc | gac | 2595 |
| | Pro | Ser | Met | Thr | Gln | Pro | Lys | Met | Tyr | Glu | Leu | Ile | Thr | Gly | Arg | Asp | |
| 30 | | | | 770 | | | | | 775 | | | | | 780 | | | |
| | tcc | gtg | cgt | gcc | acc | tac | acc | gag | gac | ctc | ctc | ggc | cgt | ggt | gac | ctc | 2643 |
| | Ser | Val | Arg | Ala | Thr | Tyr | Thr | Glu | Asp | Leu | Leu | Gly | Arg | Gly | Asp | Leu | |
| | | | 785 | | | | | 790 | | | | | 795 | | | | |
| 35 | tcc | ccc | gag | gac | gcc | gag | gcc | glt | gtc | cgc | gac | ttc | cac | gac | cag | atg | 2691 |
| | Ser | Pro | Glu | Asp | Ala | Glu | Ala | Val | Val | Arg | Asp | Phe | His | Asp | Gln | Met | |
| | 800 | | | | | 805 | | | | | 810 | | | | | | |
| 40 | gaa | tcc | gtg | ttc | aac | gag | gtc | aag | gaa | gcc | ggc | aag | aag | cag | cct | gat | 2739 |
| | Glu | Ser | Val | Phe | Asn | Glu | Val | Lys | Glu | Ala | Gly | Lys | Lys | Gln | Pro | Asp | |
| | 815 | | | | | 820 | | | | | 825 | | | | 830 | | |
| | gag | cag | acc | ggc | atc | acc | ggt | tcc | cag | gaa | ctg | acc | cgt | ggc | ctg | gac | 2787 |
| | Glu | Gln | Thr | Gly | Ile | Thr | Gly | Ser | Gln | Glu | Leu | Thr | Arg | Gly | Leu | Asp | |
| 45 | | | | | 835 | | | | | 840 | | | | 845 | | | |
| | acc | aac | atc | acc | cgc | gag | gaa | ctg | gtc | gaa | ctc | ggc | cag | gcc | ttc | gtc | 2835 |
| | Thr | Asn | Ile | Thr | Arg | Glu | Glu | Leu | Val | Glu | Leu | Gly | Gln | Ala | Phe | Val | |
| | | | | 850 | | | | | 855 | | | | | 860 | | | |
| 50 | aac | acc | cca | gag | ggc | ttc | acc | tac | cac | cca | cgt | glg | gca | ccg | gtg | gcc | 2883 |
| | Asn | Thr | Pro | Glu | Gly | Phe | Thr | Tyr | His | Pro | Arg | Val | Ala | Pro | Val | Ala | |
| | | | | 865 | | | | 870 | | | | | 875 | | | | |
| 55 | aag | aag | cgt | gcc | gag | tcc | gtc | acc | gag | ggt | ggc | atc | gac | igg | gca | igg | 2931 |
| | Lys | Lys | Arg | Ala | Glu | Ser | Val | Thr | Glu | Gly | Gly | Ile | Asp | Trp | Ala | Trp | |

| | | | | |
|----|---|------|------|------|
| | 880 | 885 | 890 | |
| | ggc gag ctc atc gcc ttc ggc tcc ctg gcc acc tcc ggc agg ctg gtc | | | 2979 |
| 5 | Gly Glu Leu Ile Ala Phe Gly Ser Leu Ala Thr Ser Gly Arg Leu Val | | | |
| | 895 | 900 | 905 | 910 |
| | cgc ctc gcc ggt gag gat tcc cgc cgt ggt acc ttc acc cag cgt cac | | | 3027 |
| | Arg Leu Ala Gly Glu Asp Ser Arg Arg Gly Thr Phe Thr Gln Arg His | | | |
| 10 | | 915 | 920 | 925 |
| | gcc gtg gcc atc gac ccg aac acc gcc gag gag ttc aac ccg ctc cac | | | 3075 |
| | Ala Val Ala Ile Asp Pro Asn Thr Ala Glu Glu Phe Asn Pro Leu His | | | |
| | 930 | 935 | 940 | |
| 15 | gag ctg gca cag gcc aag ggc ggc ggc aag ttc ctc gtc tac aac tcc | | | 3123 |
| | Glu Leu Ala Gln Ala Lys Gly Gly Gly Lys Phe Leu Val Tyr Asn Ser | | | |
| | 945 | 950 | 955 | |
| | gcg ctg acc gag tac gcg ggt atg ggc ttc gaa tac ggc tac tcc glg | | | 3171 |
| 20 | Ala Leu Thr Glu Tyr Ala Gly Met Gly Phe Glu Tyr Gly Tyr Ser Val | | | |
| | 960 | 965 | 970 | |
| | ggc aac ccg gac gcc gtg glg tcc tgg gag gca cag ttc ggt gac ttc | | | 3219 |
| | Gly Asn Pro Asp Ala Val Val Ser Trp Glu Ala Gln Phe Gly Asp Phe | | | |
| 25 | 975 | 980 | 985 | 990 |
| | gcc aac ggt gca cag acc atc atc gat gag tac atc tcc tcc ggt gag | | | 3267 |
| | Ala Asn Gly Ala Gln Thr Ile Ile Asp Glu Tyr Ile Ser Ser Gly Glu | | | |
| | 995 | 1000 | 1005 | |
| 30 | gcc aag tgg ggc cag acc tcc tcc gtc atc ctg ctg ctg ccc cac ggt | | | 3315 |
| | Ala Lys Trp Gly Gln Thr Ser Ser Val Ile Leu Leu Leu Pro His Gly | | | |
| | 1010 | 1015 | 1020 | |
| | tac gag ggc cag ggt ccg gac cac tcc tcc gca cgc atc gag cgt ttc | | | 3363 |
| 35 | Tyr Glu Gly Gln Gly Pro Asp His Ser Ser Ala Arg Ile Glu Arg Phe | | | |
| | 1025 | 1030 | 1035 | |
| | ctg cag ctg tgc gcc gag ggt tcc atg acc atc gcc cag ccg acc acc | | | 3411 |
| | Leu Gln Leu Cys Ala Glu Gly Ser Met Thr Ile Ala Gln Pro Thr Thr | | | |
| 40 | 1040 | 1045 | 1050 | |
| | ccg gcg aac tac ttc cac ctg ctg cgt cgt cac gca ctg ggc aag atg | | | 3459 |
| | Pro Ala Asn Tyr Phe His Leu Leu Arg Arg His Ala Leu Gly Lys Met | | | |
| | 1055 | 1060 | 1065 | 1070 |
| 45 | aag cgc ccg ctg gtc gtc ttc acc ccg aag tcc atg ctg cgc aac aag | | | 3507 |
| | Lys Arg Pro Leu Val Val Phe Thr Pro Lys Ser Met Leu Arg Asn Lys | | | |
| | 1075 | 1080 | 1085 | |
| | gcc gcc acc tcc gcl ccg gag gag ttc acc gag gtc acc cgc ttc aag | | | 3555 |
| 50 | Ala Ala Thr Ser Ala Pro Glu Glu Phe Thr Glu Val Thr Arg Phe Lys | | | |
| | 1090 | 1095 | 1100 | |
| | tcc gtg atc gac gat ccg aac glg gcg gat gcc tcc aag glg aag aag | | | 3603 |
| 55 | Ser Val Ile Asp Asp Pro Asn Val Ala Asp Ala Ser Lys Val Lys Lys | | | |
| | 1105 | 1110 | 1115 | |

atc atg ctg tgc tcc ggc aag atc tac tac gaa ctg gcc aag cgc aag 3651
 Ile Met Leu Cys Ser Gly Lys Ile Tyr Tyr Glu Leu Ala Lys Arg Lys

1120 1125 1130

gag aag gac aac cgc gac gac atc gcg atc gtg cgc atc gag atg ctg 3699
 Glu Lys Asp Asn Arg Asp Asp Ile Ala Ile Val Arg Ile Glu Met Leu

1135 1140 1145 1150

cac ccg atc ccg ttc aac cgt ctg cgc gac gcc ttc gac gcc tac ccc 3747
 His Pro Ile Pro Phe Asn Arg Leu Arg Asp Ala Phe Asp Gly Tyr Pro

1155 1160 1165

aac gcc gag gag atc ctg ttc gtt cag gac gag ccg gca aac cag ggt 3795
 Asn Ala Glu Glu Ile Leu Phe Val Gln Asp Glu Pro Ala Asn Gln Gly

1170 1175 1180

gcc tgg ccg ttc tac cag gag cac ctg ccc aac ctg atc gag gcc atg 3843
 Ala Trp Pro Phe Tyr Gln Glu His Leu Pro Asn Leu Ile Glu Gly Met

1185 1190 1195

ctc ccg atg cgt cgc atc tgc cgc cgt tcc cag tcc tgc act gcg acc 3891
 Leu Pro Met Arg Arg Ile Ser Arg Arg Ser Gln Ser Ser Thr Ala Thr

1200 1205 1210

ggt atc gcg aag gtc cac acc atc gag cag cag aag ctg ctg gat gat 3939
 Gly Ile Ala Lys Val His Thr Ile Glu Gln Gln Lys Leu Leu Asp Asp

1215 1220 1225 1230

gcg ttc aac gca taaacgttaa tacagcgggt galacctga accccgccgc 3991
 Ala Phe Asn Ala

acccctttaga tgcgggcggg gtttgccttt gccctgcatag gcgataatat tcatatacac 4051
 ccatcacgtt taagtctcgc atttggaatcg tgcgagcaatc ccggt 4096

<210> 34

<211> 1234

<212> PRT

<213> Corynebacterium thermoaminogenes

<400> 34

Val Ser Ser Ala Ser Thr Phe Gly Gln Asn Ala Trp Leu Val Asp Glu

1 5 10 15

Met Phe Gln Gln Phe Lys Lys Asp Pro Gln Ser Val Asp Lys Glu Trp

20 25 30

Arg Glu Leu Phe Glu Ser Gln Gly Gly Pro Gln Ala Glu Lys Ala Thr

35 40 45

Pro Ala Thr Pro Glu Ala Lys Lys Ala Ala Ser Ser Gln Ser Ser Thr

50 55 60

Ser Gly Gln Ser Thr Ala Lys Ala Ala Pro Ala Ala Lys Thr Ala Pro

65 70 75 80

Ala Ser Ala Pro Ala Lys Ala Ala Pro Val Lys Gln Asn Gln Ala Ser

| | | | | | | | |
|----|-----|-----|-----|-----|-----|-----|-----|
| | | 85 | | 90 | | 95 | |
| | Lys | Pro | Ala | Lys | Lys | Ala | Lys |
| | | | | Glu | Ser | Pro | Leu |
| | | | | | | Ser | Lys |
| | | | | | | Pro | Ala |
| | | | | | | Ala | Ala |
| 5 | | | 100 | | 105 | | 110 |
| | Met | Pro | Glu | Pro | Gly | Thr | Thr |
| | | | | Pro | Leu | Arg | Gly |
| | | | | | | Ile | Phe |
| | | | | | | Lys | Ser |
| | | | | | | Ile | |
| | | | 115 | | 120 | | 125 |
| | Ala | Lys | Asn | Met | Asp | Leu | Ser |
| | | | | Leu | Glu | Val | Pro |
| | | | | | | Thr | Ala |
| | | | | | | Thr | Ser |
| | | | | | | Val | |
| 10 | | | 130 | | 135 | | 140 |
| | Arg | Asp | Met | Pro | Ala | Arg | Leu |
| | | | | Met | Phe | Glu | Asn |
| | | | | | | Arg | Ala |
| | | | | | | Met | Val |
| | | | | | | Asn | |
| | | | 145 | | 150 | | 155 |
| | | | | | | | 160 |
| | Asp | Gln | Leu | Lys | Arg | Thr | Arg |
| | | | | Gly | Gly | Lys | Ile |
| | | | | | | Ser | Phe |
| | | | | | | Thr | His |
| | | | | | | Ile | |
| 15 | | | 165 | | 170 | | 175 |
| | Ile | Gly | Tyr | Ala | Met | Val | Lys |
| | | | | Ala | Val | Met | Ala |
| | | | | | | His | Pro |
| | | | | | | Asp | Met |
| | | | | | | Asn | |
| | | | 180 | | 185 | | 190 |
| | Asn | Ser | Tyr | Asp | Ile | Val | Asp |
| | | | | Gly | Lys | Pro | Ser |
| | | | | | | Leu | Val |
| | | | | | | Val | Pro |
| | | | | | | Glu | |
| 20 | | | 195 | | 200 | | 205 |
| | His | Ile | Asn | Leu | Gly | Leu | Ala |
| | | | | Ile | Asp | Leu | Pro |
| | | | | | | Gln | Lys |
| | | | | | | Asp | Gly |
| | | | | | | Ser | |
| | | | 210 | | 215 | | 220 |
| | Arg | Ala | Leu | Val | Val | Ala | Ala |
| | | | | Ile | Lys | Glu | Thr |
| | | | | | | Glu | Lys |
| | | | | | | Met | Thr |
| | | | | | | Phe | |
| 25 | | | 225 | | 230 | | 235 |
| | | | | | | | 240 |
| | Ser | Gln | Phe | Leu | Glu | Ala | Tyr |
| | | | | Glu | Asp | Val | Val |
| | | | | | | Ala | Arg |
| | | | | | | Ser | Arg |
| | | | | | | Val | |
| | | | | | | 245 | 250 |
| | | | | | | 255 | |
| | Gly | Lys | Leu | Thr | Met | Asp | Asp |
| | | | | Tyr | Gln | Gly | Val |
| | | | | | | Thr | Ile |
| | | | | | | Ser | Leu |
| | | | | | | Thr | |
| 30 | | | 260 | | 265 | | 270 |
| | Asn | Pro | Gly | Gly | Ile | Gly | Thr |
| | | | | Arg | His | Ser | Ile |
| | | | | | | Pro | Arg |
| | | | | | | Leu | Thr |
| | | | | | | Lys | |
| | | | 275 | | 280 | | 285 |
| | Gly | Gln | Gly | Thr | Ile | Ile | Gly |
| | | | | Val | Gly | Ser | Met |
| | | | | | | Asp | Tyr |
| | | | | | | Pro | Ala |
| | | | | | | Glu | |
| 35 | | | 290 | | 295 | | 300 |
| | Phe | Gln | Gly | Ala | Ser | Glu | Asp |
| | | | | Arg | Leu | Ala | Glu |
| | | | | | | Leu | Gly |
| | | | | | | Val | Gly |
| | | | | | | Lys | |
| | | | 305 | | 310 | | 315 |
| | | | | | | | 320 |
| | Leu | Val | Thr | Ile | Thr | Ser | Thr |
| | | | | Tyr | Asp | His | Arg |
| | | | | | | Val | Ile |
| | | | | | | Gln | Gly |
| | | | | | | Ala | |
| 40 | | | 325 | | 330 | | 335 |
| | Glu | Ser | Gly | Glu | Phe | Leu | Arg |
| | | | | Thr | Met | Ser | Gln |
| | | | | | | Leu | Leu |
| | | | | | | Val | Asp |
| | | | | | | Asp | |
| | | | 340 | | 345 | | 350 |
| | Ala | Phe | Trp | Asp | His | Ile | Phe |
| | | | | Glu | Glu | Met | Asn |
| | | | | | | Val | Pro |
| | | | | | | Tyr | Thr |
| | | | | | | Pro | |
| 45 | | | 355 | | 360 | | 365 |
| | Met | Arg | Trp | Ala | Gln | Asp | Leu |
| | | | | Pro | Asn | Thr | Gly |
| | | | | | | Val | Asp |
| | | | | | | Lys | Asn |
| | | | | | | Thr | |
| | | | 370 | | 375 | | 380 |
| | Arg | Val | Met | Gln | Leu | Ile | Glu |
| | | | | Ala | Tyr | Arg | Ser |
| | | | | | | Arg | Gly |
| | | | | | | His | Leu |
| | | | | | | Ile | |
| 50 | | | 385 | | 390 | | 395 |
| | | | | | | | 400 |
| | Ala | Asp | Thr | Asn | Pro | Leu | Pro |
| | | | | Trp | Val | Gln | Pro |
| | | | | | | Gly | Met |
| | | | | | | Pro | Val |
| | | | | | | Pro | |
| | | | | | | 405 | 410 |
| | | | | | | 415 | |
| | Asp | His | Arg | Asp | Leu | Asp | Ile |
| | | | | Glu | Thr | His | Gly |
| | | | | | | Leu | Thr |
| | | | | | | Leu | Trp |
| | | | | | | Asp | |
| 55 | | | 420 | | 425 | | 430 |

| | | | | | | | | | | | | | | | | |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| | Leu | Asp | Arg | Thr | Phe | His | Val | Gly | Gly | Phe | Gly | Gly | Lys | Glu | Thr | Met |
| | | 435 | | | | | | 440 | | | | | 445 | | | |
| 5 | Thr | Leu | Arg | Glu | Val | Leu | Ser | Arg | Leu | Arg | Ala | Ala | Tyr | Thr | Leu | Lys |
| | | 450 | | | | | 455 | | | | | 460 | | | | |
| | Val | Gly | Ser | Glu | Tyr | Thr | His | Ile | Leu | Asp | Arg | Asp | Glu | Arg | Thr | Trp |
| | 465 | | | | | 470 | | | | 475 | | | | | | 480 |
| 10 | Leu | Gln | Asp | Arg | Leu | Glu | Ala | Gly | Met | Pro | Lys | Pro | Thr | Ala | Ala | Glu |
| | | | | | 485 | | | | 490 | | | | | | | 495 |
| | Gln | Lys | Tyr | Ile | Leu | Gln | Lys | Leu | Asn | Ala | Ala | Glu | Ala | Phe | Glu | Asn |
| | | | | 500 | | | | | 505 | | | | | 510 | | |
| 15 | Phe | Leu | Gln | Thr | Lys | Tyr | Val | Gly | Gln | Lys | Arg | Phe | Ser | Leu | Glu | Gly |
| | | 515 | | | | | | 520 | | | | | 525 | | | |
| | Ala | Glu | Ser | Leu | Ile | Pro | Leu | Met | Asp | Ser | Ala | Ile | Asp | Thr | Ala | Ala |
| | | 530 | | | | | 535 | | | | | 540 | | | | |
| 20 | Gly | Gln | Gly | Leu | Asp | Glu | Val | Val | Ile | Gly | Met | Pro | His | Arg | Gly | Arg |
| | 545 | | | | | 550 | | | | | 555 | | | | | 560 |
| | Leu | Asn | Val | Leu | Phe | Asn | Ile | Val | Gly | Lys | Pro | Leu | Ala | Ser | Ile | Phe |
| | | | | | 565 | | | | | 570 | | | | | | 575 |
| 25 | Asn | Glu | Phe | Glu | Gly | Gln | Met | Glu | Gln | Gly | Gln | Ile | Gly | Gly | Ser | Gly |
| | | | 580 | | | | | | 585 | | | | | 590 | | |
| | Asp | Val | Lys | Tyr | His | Leu | Gly | Ser | Glu | Gly | Thr | His | Leu | Gln | Met | Phe |
| | | 595 | | | | | | 600 | | | | | 605 | | | |
| 30 | Gly | Asp | Gly | Glu | Ile | Lys | Val | Ser | Leu | Thr | Ala | Asn | Pro | Ser | His | Leu |
| | | 610 | | | | | 615 | | | | | 620 | | | | |
| | Glu | Ala | Val | Asn | Pro | Val | Val | Glu | Gly | Ile | Val | Arg | Ala | Lys | Gln | Asp |
| | 625 | | | | | 630 | | | | | 635 | | | | | 640 |
| 35 | Ile | Leu | Asp | Lys | Gly | Pro | Asp | Gly | Tyr | Thr | Val | Val | Pro | Leu | Leu | Leu |
| | | | | | 645 | | | | 650 | | | | | | 655 | |
| | His | Gly | Asp | Ala | Ala | Phe | Ala | Gly | Leu | Gly | Ile | Val | Pro | Glu | Thr | Ile |
| | | | 660 | | | | | | 665 | | | | | 670 | | |
| 40 | Asn | Leu | Ala | Ala | Leu | Arg | Gly | Tyr | Asp | Val | Gly | Gly | Thr | Ile | His | Ile |
| | | 675 | | | | | | 680 | | | | | 685 | | | |
| | Val | Val | Asn | Asn | Gln | Ile | Gly | Phe | Thr | Thr | Thr | Pro | Asp | Ser | Ser | Arg |
| | | 690 | | | | | 695 | | | | | 700 | | | | |
| 45 | Ser | Met | His | Tyr | Ala | Thr | Asp | Cys | Ala | Lys | Ala | Phe | Gly | Cys | Pro | Val |
| | 705 | | | | | 710 | | | | | 715 | | | | | 720 |
| | Phe | His | Val | Asn | Gly | Asp | Asp | Pro | Glu | Ala | Val | Val | Trp | Val | Gly | Gln |
| | | | | | 725 | | | | | 730 | | | | | 735 | |
| 50 | Leu | Ala | Thr | Glu | Tyr | Arg | Arg | Arg | Phe | Gly | Lys | Asp | Val | Phe | Ile | Asp |
| | | | 740 | | | | | | 745 | | | | | 750 | | |
| | Leu | Ile | Cys | Tyr | Arg | Leu | Arg | Gly | His | Asn | Glu | Ala | Asp | Asp | Pro | Ser |
| | | 755 | | | | | | 760 | | | | | 765 | | | |
| 55 | Met | Thr | Gln | Pro | Lys | Met | Tyr | Glu | Leu | Ile | Thr | Gly | Arg | Asp | Ser | Val |

770 775 780
 Arg Ala Thr Tyr Thr Glu Asp Leu Leu Gly Arg Gly Asp Leu Ser Pro
 785 790 795 800
 Glu Asp Ala Glu Ala Val Val Arg Asp Phe His Asp Gln Met Glu Ser
 805 810 815
 Val Phe Asn Glu Val Lys Glu Ala Gly Lys Lys Gln Pro Asp Glu Gln
 820 825 830
 Thr Gly Ile Thr Gly Ser Gln Glu Leu Thr Arg Gly Leu Asp Thr Asn
 835 840 845
 Ile Thr Arg Glu Glu Leu Val Glu Leu Gly Gln Ala Phe Val Asn Thr
 850 855 860
 Pro Glu Gly Phe Thr Tyr His Pro Arg Val Ala Pro Val Ala Lys Lys
 865 870 875 880
 Arg Ala Glu Ser Val Thr Glu Gly Gly Ile Asp Trp Ala Trp Gly Glu
 885 890 895
 Leu Ile Ala Phe Gly Ser Leu Ala Thr Ser Gly Arg Leu Val Arg Leu
 900 905 910
 Ala Gly Glu Asp Ser Arg Arg Gly Thr Phe Thr Gln Arg His Ala Val
 915 920 925
 Ala Ile Asp Pro Asn Thr Ala Glu Glu Phe Asn Pro Leu His Glu Leu
 930 935 940
 Ala Gln Ala Lys Gly Gly Gly Lys Phe Leu Val Tyr Asn Ser Ala Leu
 945 950 955 960
 Thr Glu Tyr Ala Gly Met Gly Phe Glu Tyr Gly Tyr Ser Val Gly Asn
 965 970 975
 Pro Asp Ala Val Val Ser Trp Glu Ala Gln Phe Gly Asp Phe Ala Asn
 980 985 990
 Gly Ala Gln Thr Ile Ile Asp Glu Tyr Ile Ser Ser Gly Glu Ala Lys
 995 1000 1005
 Trp Gly Gln Thr Ser Ser Val Ile Leu Leu Leu Pro His Gly Tyr Glu
 1010 1015 1020
 Gly Gln Gly Pro Asp His Ser Ser Ala Arg Ile Glu Arg Phe Leu Gln
 1025 1030 1035 1040
 Leu Cys Ala Glu Gly Ser Met Thr Ile Ala Gln Pro Thr Thr Pro Ala
 1045 1050 1055
 Asn Tyr Phe His Leu Leu Arg Arg His Ala Leu Gly Lys Met Lys Arg
 1060 1065 1070
 Pro Leu Val Val Phe Thr Pro Lys Ser Met Leu Arg Asn Lys Ala Ala
 1075 1080 1085
 Thr Ser Ala Pro Glu Glu Phe Thr Glu Val Thr Arg Phe Lys Ser Val
 1090 1095 1100
 Ile Asp Asp Pro Asn Val Ala Asp Ala Ser Lys Val Lys Lys Ile Met
 105 110 1115 1120

Leu Cys Ser Gly Lys Ile Tyr Tyr Glu Leu Ala Lys Arg Lys Glu Lys
 1125 1130 1135

5 Asp Asn Arg Asp Asp Ile Ala Ile Val Arg Ile Glu Met Leu His Pro
 1140 1145 1150
 Ile Pro Phe Asn Arg Leu Arg Asp Ala Phe Asp Gly Tyr Pro Asn Ala
 1155 1160 1165
 10 Glu Glu Ile Leu Phe Val Gln Asp Glu Pro Ala Asn Gln Gly Ala Trp
 1170 1175 1180
 Pro Phe Tyr Gln Glu His Leu Pro Asn Leu Ile Glu Gly Met Leu Pro
 185 1190 1195 1200
 15 Met Arg Arg Ile Ser Arg Arg Ser Gln Ser Ser Thr Ala Thr Gly Ile
 1205 1210 1215
 Ala Lys Val His Thr Ile Glu Gln Gln Lys Leu Leu Asp Asp Ala Phe
 1220 1225 1230
 20 Asn Ala

<210> 35
 <211> 20
 25 <212> DNA
 <213> Artificial Sequence

<220>
 30 <223> Description of Artificial Sequence: primer for aceA

<400> 35
 35 ccctaccca gcgaactcgg 20

<210> 36
 <211> 20
 40 <212> DNA
 <213> Artificial Sequence

<220>
 45 <223> Description of Artificial Sequence: primer for aceA

<400> 36
 50 ctgcccttgaa ctcacggttc 20

<210> 37
 <211> 20
 55 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for accBC

5 <400> 37

catccacccc ggclacggct

20

10 <210> 38

<211> 20

<212> DNA

<213> Artificial Sequence

15 <220>

<223> Description of Artificial Sequence: primer for accBC

20 <400> 38

cggtagcagg ggtgccacc

20

<210> 39

25 <211> 20

<212> DNA

<213> Artificial Sequence

30 <220>

<223> Description of Artificial Sequence: primer for disR1

<400> 39

35 acgccccagc cctgaccgac

20

<210> 40

<211> 20

40 <212> DNA

<213> Artificial Sequence

<220>

45 <223> Description of Artificial Sequence: primer for disR1

<400> 40

50 agcagcgccc atgacggcga

20

<210> 41

<211> 20

55 <212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for dlsR2

5

<400> 41

acggcccagc cctgaccgac

20

10

<210> 42

<211> 20

<212> DNA

<213> Artificial Sequence

15

<220>

<223> Description of Artificial Sequence: primer for dlsR2

20

<400> 42

agcagcgccc atgacggcga

20

25

<210> 43

<211> 20

<212> DNA

<213> Artificial Sequence

30

<220>

<223> Description of Artificial Sequence: primer for pfk

35

<400> 43

cgicalccga ggaatcgtcc

20

40

<210> 44

<211> 20

<212> DNA

<213> Artificial Sequence

45

<220>

<223> Description of Artificial Sequence: primer for pfk

50

<400> 44

cgtggcggcc catgacctcc

21

55

<210> 45

<211> 17

<212> DNA

5 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: primer for scrB
 <220>
 10 <221> UNSURE
 <222> (3)
 <223> n=a or g or c or t
 15 <400> 45
 ggncghytba aygaycc 17
 <210> 46
 20 <211> 20
 <212> DNA
 <213> Artificial Sequence
 25 <220>
 <223> Description of Artificial Sequence: primer for scrB
 <220>
 30 <221> UNSURE
 <222> (18)
 <223> n=a or g or c or t
 35 <400> 46
 ggrcaytccc acatrtance 20
 <210> 47
 40 <211> 20
 <212> DNA
 <213> Artificial Sequence
 45 <220>
 <223> Description of Artificial Sequence: primer for gluABCD
 <400> 47
 50 ccatccggat ccggcaagtc 20
 <210> 48
 55 <211> 20
 <212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for gluABCD

<400> 48

aatcccatct cgtggglaac

20

<210> 49

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for pdhA

<400> 49

acigtgtcca tgggtcttgg ccc

23

<210> 50

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for pdhA

<400> 50

cgctggaatccgaacatcga

20

<210> 51

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for pc

<400> 51

ggcgcaacct acgacgttgc aatgcg

26

<210> 52

<211> 20

<212> DNA

<213> Artificial Sequence

5

<220>

<223> Description of Artificial Sequence: primer for pc

10

<400> 52

tgccgcctg ggtatcgtg

20

<210> 53

<211> 20

15

<212> DNA

<213> Artificial Sequence

20

<220>

<223> Description of Artificial Sequence: primer for ppc

<400> 53

ggatccgga ttgtggaga

20

25

<210> 54

<211> 20

30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for ppc

35

<400> 54

ccgccatcct tgttgaatc

20

40

<210> 55

<211> 20

<212> DNA

45

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for acn

50

<220>

<221> UNSURE

<222> (3,6,9)

55

<223> n=inosine

<400> 55

gtingnacng aylcscalac

20

<210> 56

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for acn

<220>

<221> UNSURE

<222> (3, 9, 18)

<223> n=inosine

<400> 56

gcnggagana tgtgrlcngt

20

<210> 57

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for icd

<400> 57

gacallcac lcgclggacg

20

<210> 58

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for icd

<400> 58

ccglacitit cagccititg

20

<210> 59

<211> 17
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer for lpd

<400> 59
 atcatcgcaa ccggttc

17

<210> 60
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer for lpd

<400> 60
 cgtcaccgat ggcgtaaat

19

<210> 61
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer for odhA

<400> 61
 acaccgtggc cgcccaacg

20

<210> 62
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer for odhA

<400> 62
 tgctaaccgc tcccacctgg

20

<210> 63

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for
screening PCR of lpd

<400> 63

tacgaggagc agatccctcaa

20

<210> 64

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for
screening PCR of lpd

<400> 64

ttgacgccgg tgtctccag

20

<210> 65

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for
LA cloning of acn

<400> 65

ggtgaagcta agtagttagc

20

<210> 66

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for

LA cloning of acn

5 <400> 66
agctactaaa cctgcacc 18

<210> 67
10 <211> 20
<212> DNA
<213> Artificial Sequence

15 <220>
<223> Description of Artificial Sequence: primer for
LA cloning of icd

20 <400> 67
ccgtactctt cagccttcg 67

<210> 68
25 <211> 18
<212> DNA
<213> Artificial Sequence

30 <220>
<223> Description of Artificial Sequence: primer for
LA cloning of icd

35 <400> 68
tcgtccttgt tccacatc 18

<210> 69
40 <211> 17
<212> DNA
<213> Artificial Sequence

45 <220>
<223> Description of Artificial Sequence: primer for
LA cloning of lpd

50 <400> 69
atcatcgcaa ccggttc 17

55 <210> 70
<211> 20

<212> DNA

<213> Artificial Sequence

5 <220>

<223> Description of Artificial Sequence: primer for
LA cloning of lpd

10 <400> 70

tacgaggagc agatccctcaa

20

15 <210> 71

<211> 20

<212> DNA

<213> Artificial Sequence

20 <220>

<223> Description of Artificial Sequence: primer for
LA cloning of acn

25 <400> 71

gctaaactact tagcttcacc

20

30 <210> 72

<211> 20

<212> DNA

<213> Artificial Sequence

35 <220>

<223> Description of Artificial Sequence: primer for
LA cloning of acn

40 <400> 72

gaaccaggaa ctattgaacc

20

45 <210> 73

<211> 18

<212> DNA

<213> Artificial Sequence

50 <220>

<223> Description of Artificial Sequence: primer for
LA cloning of icd

<400> 73

tccgatgtca tcatcgac

18

<210> 74

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for
LA cloning of icd

<400> 74

atgtggaaca aggacgac

18

<210> 75

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for
LA cloning of odhA

<400> 75

gtacatatgt tcgttagaac gcgtaatacg acica

35

<210> 76

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for
LA cloning of odhA

<400> 76

cglttagaacg cglaatacga ctactatag ggaga

35

<210> 77

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer for
amplifying gdh gene

<400> 77

gcgccatgcag gtccgagggt gtgcgttcgg ca

32

<210> 78

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer for
amplifying gdh gene

<400> 78

gcgccatgcag ccaccagga tgcctcaacc ag

32

<210> 79

<211> 1344

<212> DNA

<213> Corynebacterium thermoaminogenes

<220>

<221> CDS

<222> (1)..(1341)

<400> 79

atg act gta gat gag cag gtc tcc aac tac tac gac atg ctg ctg aag 48

Met Thr Val Asp Glu Gln Val Ser Asn Tyr Tyr Asp Met Leu Leu Lys

1 5 10 15

cgc aac gcc ggg gaa cct gag ttc cac cag gct gtc gcg gag gtt ctc 96

Arg Asn Ala Gly Glu Pro Glu Phe His Gln Ala Val Ala Glu Val Leu

20 25 30

gaa tct ctg aag atc gtc ctg gag aag gac ccg cac tac gcc gac tac 144

Glu Ser Leu Lys Ile Val Leu Glu Lys Asp Pro His Tyr Ala Asp Tyr

35 40 45

ggc ctg atc cag cgt ctc tgc gaa ccg gaa cgc cag ctg atc ttc cgt 192

5

10

15

20

25

30

35

40

45

50

55

| | | | | |
|----|---|-----|-----|------|
| | 275 | 280 | 285 | |
| | gca cgc glg tcc tcc tac gcc gac gag glg gag ggt gcg gag tac cac | | | 912 |
| 5 | Ala Arg Val Ser Ser Tyr Ala Asp Glu Val Glu Gly Ala Glu Tyr His | | | |
| | 290 | 295 | 300 | |
| | acc gac ggc tcc atc tgg gat ctg acc gcc gac atc gcg ctg ccc tgc | | | 960 |
| | Thr Asp Gly Ser Ile Trp Asp Leu Thr Ala Asp Ile Ala Leu Pro Cys | | | |
| 10 | 305 | 310 | 315 | 320 |
| | gcc acc cag aac gaa ctg gac ggc gac aac gcc cgc acc ctg gcg gac | | | 1008 |
| | Ala Thr Gln Asn Glu Leu Asp Gly Asp Asn Ala Arg Thr Leu Ala Asp | | | |
| | 325 | 330 | 335 | |
| 15 | aac ggc tgc cgc ttc gtg gcg gag ggc gcc aac atg ccc tcc acc ccc | | | 1056 |
| | Asn Gly Cys Arg Phe Val Ala Glu Gly Ala Asn Met Pro Ser Thr Pro | | | |
| | 340 | 345 | 350 | |
| | gag gcc atc gac gtc ttc cgt gag cgt ggt gtt ctg ttc ggg cgg ggc | | | 1104 |
| 20 | Glu Ala Ile Asp Val Phe Arg Glu Arg Gly Val Leu Phe Gly Pro Gly | | | |
| | 355 | 360 | 365 | |
| | aag gct gcc aac gcc ggt ggc gtg gcc acc tcc gcc ctg gag atg cag | | | 1152 |
| | Lys Ala Ala Asn Ala Gly Gly Val Ala Thr Ser Ala Leu Glu Met Gln | | | |
| 25 | 370 | 375 | 380 | |
| | cag aac gcc tcc cgt gat tcc tgg agc ttc gag tac acc gat gag cgt | | | 1200 |
| | Gln Asn Ala Ser Arg Asp Ser Trp Ser Phe Glu Tyr Thr Asp Glu Arg | | | |
| | 385 | 390 | 395 | 400 |
| 30 | ctc cac cgc atc atg aag aac atc ttc aag tcc tgc gcc gat acc gcc | | | 1248 |
| | Leu His Arg Ile Met Lys Asn Ile Phe Lys Ser Cys Ala Asp Thr Ala | | | |
| | 405 | 410 | 415 | |
| | aag gag tac ggc cac gag aag aac tac gtg gtc ggt gcg aac atc gcc | | | 1296 |
| 35 | Lys Glu Tyr Gly His Glu Lys Asn Tyr Val Val Gly Ala Asn Ile Ala | | | |
| | 420 | 425 | 430 | |
| | gga ttc aag aag gtc gct gac gcc atg ctg gcc cag ggt gtc atc taa | | | 1344 |
| | Gly Phe Lys Lys Val Ala Asp Ala Met Leu Ala Gln Gly Val Ile | | | |
| 40 | 435 | 440 | 445 | |
| | <210> 80 | | | |
| | <211> 447 | | | |
| 45 | <212> PRT | | | |
| | <213> Corynebacterium thermoaminogenes | | | |
| | <400> 80 | | | |
| 50 | Met Thr Val Asp Glu Gln Val Ser Asn Tyr Tyr Asp Met Leu Leu Lys | | | |
| | 1 5 10 15 | | | |
| | Arg Asn Ala Gly Glu Pro Glu Phe His Gln Ala Val Ala Glu Val Leu | | | |
| | 20 25 30 | | | |
| 55 | Glu Ser Leu Lys Ile Val Leu Glu Lys Asp Pro His Tyr Ala Asp Tyr | | | |

35 40 45
 Gly Leu Ile Gln Arg Leu Cys Glu Pro Glu Arg Gln Leu Ile Phe Arg
 50 55 60
 5 Val Pro Trp Val Asp Asp Asn Gly Gln Val His Val Asn Arg Gly Phe
 65 70 75 80
 Arg Val Gln Phe Asn Ser Ala Leu Gly Pro Tyr Lys Gly Gly Leu Arg
 85 90 95
 10 Phe His Pro Ser Val Asn Leu Gly Ile Val Lys Phe Leu Gly Phe Glu
 100 105 110
 Gln Ile Phe Lys Asn Ser Leu Thr Gly Leu Pro Ile Gly Gly Gly Lys
 115 120 125
 15 Gly Gly Ser Asp Phe Asp Pro Lys Gly Lys Ser Glu Leu Glu Ile Met
 130 135 140
 Arg Phe Cys Gln Ser Phe Met Thr Glu Leu His Arg His Ile Gly Glu
 145 150 155 160
 20 Tyr Arg Asp Val Pro Ala Gly Asp Ile Gly Val Gly Gly Arg Glu Ile
 165 170 175
 Gly Tyr Leu Phe Gly His Tyr Arg Arg Leu Ala Asn Gln His Glu Ser
 180 185 190
 25 Gly Val Leu Thr Gly Lys Gly Leu Thr Trp Gly Gly Ser Leu Val Arg
 195 200 205
 Thr Glu Ala Thr Gly Phe Gly Thr Val Tyr Phe Val Gln Glu Met Ile
 210 215 220
 30 Lys Ala Glu Gly Glu Thr Leu Glu Gly Lys Lys Val Ile Val Ser Gly
 225 230 235 240
 Ser Gly Asn Val Ala Thr Tyr Ala Ile Gln Lys Val Gln Glu Leu Gly
 245 250 255
 35 Ala Val Val Val Gly Phe Ser Asp Ser Ser Gly Trp Val Ser Thr Pro
 260 265 270
 Asn Gly Val Asp Val Ala Lys Leu Arg Glu Ile Lys Glu Val Arg Arg
 275 280 285
 40 Ala Arg Val Ser Ser Tyr Ala Asp Glu Val Glu Gly Ala Glu Tyr His
 290 295 300
 Thr Asp Gly Ser Ile Trp Asp Leu Thr Ala Asp Ile Ala Leu Pro Cys
 305 310 315 320
 45 Ala Thr Gln Asn Glu Leu Asp Gly Asp Asn Ala Arg Thr Leu Ala Asp
 325 330 335
 Asn Gly Cys Arg Phe Val Ala Glu Gly Ala Asn Met Pro Ser Thr Pro
 340 345 350
 50 Glu Ala Ile Asp Val Phe Arg Glu Arg Gly Val Leu Phe Gly Pro Gly
 355 360 365
 Lys Ala Ala Asn Ala Gly Gly Val Ala Thr Ser Ala Leu Glu Met Gln
 370 375 380
 55

Gln Asn Ala Ser Arg Asp Ser Trp Ser Phe Glu Tyr Thr Asp Glu Arg
385 390 395 400

Leu His Arg Ile Met Lys Asn Ile Phe Lys Ser Cys Ala Asp Thr Ala
405 410 415

Lys Glu Tyr Gly His Glu Lys Asn Tyr Val Val Gly Ala Asn Ile Ala
420 425 430

Gly Phe Lys Lys Val Ala Asp Ala Met Leu Ala Gln Gly Val Ile
435 440 445

<210> 81

<211> 1344

<212> DNA

<213> Brevibacterium lactofermentum

<220>

<221> CDS

<222> (1)..(1341)

<400> 81

atg aca gtt gat gag cag gtc tct aac tat tac gac atg ctt ctg aag 48

Met. Thr. Val. Asp. Glu. Gln. Val. Ser. Asn. Tyr. Tyr. Asp. Met. Leu. Leu. Lys.

1 5 10 15

cgc aat gct ggc gag cct gaa ttt cac cag gca gtg gca gag gtt ttg 96

Arg. Asn. Ala. Gly. Glu. Pro. Glu. Phe. His. Gln. Ala. Val. Ala. Glu. Val. Leu.

20 25 30

gaa tct ttg aag atc gtc ctg gaa aag gac cct cat tac gct gat tac 144

Glu. Ser. Leu. Lys. Ile. Val. Leu. Glu. Lys. Asp. Pro. His. Tyr. Ala. Asp. Tyr.

35 40 45

ggt ctc atc cag cgc ctg tgc gag cct gag cgt cag ctc atc ttc cgt 192

Gly. Leu. Ile. Gln. Arg. Leu. Cys. Glu. Pro. Glu. Arg. Gln. Leu. Ile. Phe. Arg.

50 55 60

gtg cct lgg gtt gat gac cag ggc cag gtc cac gtc aac cgt ggt ttc 240

Val. Pro. Trp. Val. Asp. Asp. Gln. Gly. Gln. Val. His. Val. Asn. Arg. Gly. Phe.

65 70 75 80

cgc gtc cag ttc aac tct gca ctt gga cca tac aag ggc ggc ctg cgc 288

Arg. Val. Gln. Phe. Asn. Ser. Ala. Leu. Gly. Pro. Tyr. Lys. Gly. Gly. Leu. Arg.

85 90 95

ttc cac cca tct gta aac ctg ggc att gtg aag ttc ctg ggc ttt gag 336

Phe. His. Pro. Ser. Val. Asn. Leu. Gly. Ile. Val. Lys. Phe. Leu. Gly. Phe. Glu.

100 105 110

cag atc ttt aaa aac tcc cta acc ggc ctg cca atc ggt ggt ggc aag 384

Gln. Ile. Phe. Lys. Asn. Ser. Leu. Thr. Gly. Leu. Pro. Ile. Gly. Gly. Gly. Lys.

115 120 125

| | | |
|----|---|------|
| | ggl gga tcc gac ttc gac cct aag ggc aag tcc gat ctg gaa atc atg | 432 |
| | Gly Gly Ser Asp Phe Asp Pro Lys Gly Lys Ser Asp Leu Glu Ile Met | |
| | 130 135 140 | |
| 5 | cgt ttc tgc cag tcc ttc atg acc gag ctg cac cgc cac atc ggt gag | 480 |
| | Arg Phe Cys Gln Ser Phe Met Thr Glu Leu His Arg His Ile Gly Glu | |
| | 145 150 155 160 | |
| 10 | tac cgc gac gtt cct gca ggt gac atc gga gtt ggt ggc cgc gag atc | 528 |
| | Tyr Arg Asp Val Pro Ala Gly Asp Ile Gly Val Gly Gly Arg Glu Ile | |
| | 165 170 175 | |
| | ggt tac ctg ttt ggc cac tac cgt cgc atg gct aac cag cac gag tcc | 576 |
| 15 | Gly Tyr Leu Phe Gly His Tyr Arg Arg Met Ala Asn Gln His Glu Ser | |
| | 180 185 190 | |
| | ggc gtt ttg acc ggt aag ggc ctg acc tgg ggt gga tcc ctg gtc cgc | 624 |
| | Gly Val Leu Thr Gly Lys Gly Leu Thr Trp Gly Gly Ser Leu Val Arg | |
| 20 | 195 200 205 | |
| | acc gag gca act ggc tac ggc tgc gtt tac ttc gtg agt gaa atg atc | 672 |
| | Thr Glu Ala Thr Gly Tyr Gly Cys Val Tyr Phe Val Ser Glu Met Ile | |
| | 210 215 220 | |
| 25 | aag gct aag ggc gag agc atc agc ggc cag aag atc atc gtt tcc ggt | 720 |
| | Lys Ala Lys Gly Glu Ser Ile Ser Gly Gln Lys Ile Ile Val Ser Gly | |
| | 225 230 235 240 | |
| | tcc ggc aac gla gca acc tac gcg att gaa aag gct cag gaa ctc ggc | 768 |
| 30 | Ser Gly Asn Val Ala Thr Tyr Ala Ile Glu Lys Ala Gln Glu Leu Gly | |
| | 245 250 255 | |
| | gca acc gtt att ggt ttc tcc gat tcc agc ggt tgg gtt cat acc cct | 816 |
| 35 | Ala Thr Val Ile Gly Phe Ser Asp Ser Ser Gly Trp Val His Thr Pro | |
| | 260 265 270 | |
| | aac ggc gtt gac gtg gct aag ctc cgc gaa atc aag gaa gtt cgc cgc | 864 |
| | Asn Gly Val Asp Val Ala Lys Leu Arg Glu Ile Lys Glu Val Arg Arg | |
| | 275 280 285 | |
| 40 | gca cgc gla tcc gtg tac gcc gac gaa att gaa ggc gca acc tac cac | 912 |
| | Ala Arg Val Ser Val Tyr Ala Asp Glu Ile Glu Gly Ala Thr Tyr His | |
| | 290 295 300 | |
| 45 | acc gac ggt tcc atc tgg gat ctc aag tgc gat atc gct ctt cct tgt | 960 |
| | Thr Asp Gly Ser Ile Trp Asp Leu Lys Cys Asp Ile Ala Leu Pro Cys | |
| | 305 310 315 320 | |
| | gca act cag aac gag ctc aac ggc gag aac gct aag act ctt gca gac | 1008 |
| 50 | Ala Thr Gln Asn Glu Leu Asn Gly Glu Asn Ala Lys Thr Leu Ala Asp | |
| | 325 330 335 | |
| | aac ggc tgc cgt ttc gtt gct gaa ggc gcg aac atg cct tcc acc cct | 1056 |
| | Asn Gly Cys Arg Phe Val Ala Glu Gly Ala Asn Met Pro Ser Thr Pro | |
| | 340 345 350 | |
| 55 | gag gct gtt gag gtc ttc cgt gag cgc gac atc cgc ttc gga cca ggc | 1104 |

EP 1 219 712 A1

| | | | | | | | | | | | | | | | | | |
|----|-------------------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| | Glu | Ala | Val | Glu | Val | Phe | Arg | Glu | Arg | Asp | Ile | Arg | Phe | Gly | Pro | Gly | |
| | 355 | | | | | | 360 | | | | | | 365 | | | | |
| 5 | aag | gca | gct | aac | gct | ggt | ggc | ggt | gca | acc | tcc | gct | ctg | gag | atg | cag | 1152 |
| | Lys | Ala | Ala | Asn | Ala | Gly | Gly | Val | Ala | Thr | Ser | Ala | Leu | Glu | Met | Gln | |
| | 370 | | | | | | 375 | | | | | | 380 | | | | |
| 10 | cag | aac | gct | tcg | cgc | gat | tcc | tgg | agc | ttc | gag | lac | acc | gac | gag | cgc | 1200 |
| | Gln | Asn | Ala | Ser | Arg | Asp | Ser | Trp | Ser | Phe | Glu | Tyr | Thr | Asp | Glu | Arg | |
| | 385 | | | | | | 390 | | | | | | 395 | | | 400 | |
| | ctc | cag | gtg | atc | atg | aag | aac | atc | ttc | aag | acc | tgt | gca | gag | acc | gca | 1248 |
| | Leu | Gln | Val | Ile | Met | Lys | Asn | Ile | Phe | Lys | Thr | Cys | Ala | Glu | Thr | Ala | |
| 15 | | | | 405 | | | | | | 410 | | | | | | 415 | |
| | gca | gag | tat | gga | cac | gag | aac | gat | tac | gtt | gtc | ggc | gct | aac | att | gct | 1296 |
| | Ala | Glu | Tyr | Gly | His | Glu | Asn | Asp | Tyr | Val | Val | Gly | Ala | Asn | Ile | Ala | |
| | | | | 420 | | | | | | 425 | | | | | | 430 | |
| 20 | ggc | ttt | aag | aag | gta | gct | gac | gcg | atg | ctg | gca | cag | ggc | gtc | atc | taa | 1344 |
| | Gly | Phe | Lys | Lys | Val | Ala | Asp | Ala | Met | Leu | Ala | Gln | Gly | Val | Ile | | |
| | 435 | | | | | | 440 | | | | | | 445 | | | | |
| 25 | <210> 82 | | | | | | | | | | | | | | | | |
| | <211> 447 | | | | | | | | | | | | | | | | |
| | <212> PRT | | | | | | | | | | | | | | | | |
| | <213> Brevibacterium lactofermentum | | | | | | | | | | | | | | | | |
| 30 | <400> 82 | | | | | | | | | | | | | | | | |
| | Met | Thr | Val | Asp | Glu | Gln | Val | Ser | Asn | Tyr | Tyr | Asp | Met | Leu | Leu | Lys | |
| | 1 | | | | 5 | | | | | 10 | | | | | 15 | | |
| 35 | Arg | Asn | Ala | Gly | Glu | Pro | Glu | Phe | His | Gln | Ala | Val | Ala | Glu | Val | Leu | |
| | 20 | | | | | | 25 | | | | | | 30 | | | | |
| | Glu | Ser | Leu | Lys | Ile | Val | Leu | Glu | Lys | Asp | Pro | His | Tyr | Ala | Asp | Tyr | |
| | 35 | | | | | | 40 | | | | | | 45 | | | | |
| 40 | Gly | Leu | Ile | Gln | Arg | Leu | Cys | Glu | Pro | Glu | Arg | Gln | Leu | Ile | Phe | Arg | |
| | 50 | | | | | | 55 | | | | | | 60 | | | | |
| | Val | Pro | Trp | Val | Asp | Asp | Gln | Gly | Gln | Val | His | Val | Asn | Arg | Gly | Phe | |
| | 65 | | | | | | 70 | | | | | | 75 | | | 80 | |
| 45 | Arg | Val | Gln | Phe | Asn | Ser | Ala | Leu | Gly | Pro | Tyr | Lys | Gly | Gly | Leu | Arg | |
| | | | | 85 | | | | | | 90 | | | | | | 95 | |
| | Phe | His | Pro | Ser | Val | Asn | Leu | Gly | Ile | Val | Lys | Phe | Leu | Gly | Phe | Glu | |
| | 100 | | | | | | 105 | | | | | | 110 | | | | |
| 50 | Gln | Ile | Phe | Lys | Asn | Ser | Leu | Thr | Gly | Leu | Pro | Ile | Gly | Gly | Gly | Lys | |
| | 115 | | | | | | 120 | | | | | | 125 | | | | |
| | Gly | Gly | Ser | Asp | Phe | Asp | Pro | Lys | Gly | Lys | Ser | Asp | Leu | Glu | Ile | Met | |
| | 130 | | | | | | 135 | | | | | | 140 | | | | |
| 55 | Arg | Phe | Cys | Gln | Ser | Phe | Met | Thr | Glu | Leu | His | Arg | His | Ile | Gly | Glu | |

145 150 155 160
 Tyr Arg Asp Val Pro Ala Gly Asp Ile Gly Val Gly Gly Arg Glu Ile
 165 170 175
 5 Gly Tyr Leu Phe Gly His Tyr Arg Arg Met Ala Asn Gln His Glu Ser
 180 185 190
 Gly Val Leu Thr Gly Lys Gly Leu Thr Trp Gly Gly Ser Leu Val Arg
 195 200 205
 10 Thr Glu Ala Thr Gly Tyr Gly Cys Val Tyr Phe Val Ser Glu Met Ile
 210 215 220
 Lys Ala Lys Gly Glu Ser Ile Ser Gly Gln Lys Ile Ile Val Ser Gly
 15 225 230 235 240
 Ser Gly Asn Val Ala Thr Tyr Ala Ile Glu Lys Ala Gln Glu Leu Gly
 245 250 255
 Ala Thr Val Ile Gly Phe Ser Asp Ser Ser Gly Trp Val His Thr Pro
 20 260 265 270
 Asn Gly Val Asp Val Ala Lys Leu Arg Glu Ile Lys Glu Val Arg Arg
 275 280 285
 Ala Arg Val Ser Val Tyr Ala Asp Glu Ile Glu Gly Ala Thr Tyr His
 25 290 295 300
 Thr Asp Gly Ser Ile Trp Asp Leu Lys Cys Asp Ile Ala Leu Pro Cys
 305 310 315 320
 Ala Thr Gln Asn Glu Leu Asn Gly Glu Asn Ala Lys Thr Leu Ala Asp
 30 325 330 335
 Asn Gly Cys Arg Phe Val Ala Glu Gly Ala Asn Met Pro Ser Thr Pro
 340 345 350
 Glu Ala Val Glu Val Phe Arg Glu Arg Asp Ile Arg Phe Gly Pro Gly
 35 355 360 365
 Lys Ala Ala Asn Ala Gly Gly Val Ala Thr Ser Ala Leu Glu Met Gln
 370 375 380
 Gln Asn Ala Ser Arg Asp Ser Trp Ser Phe Glu Tyr Thr Asp Glu Arg
 40 385 390 395 400
 Leu Gln Val Ile Met Lys Asn Ile Phe Lys Thr Cys Ala Glu Thr Ala

 405 410 415
 45 Ala Glu Tyr Gly His Glu Asn Asp Tyr Val Val Gly Ala Asn Ile Ala
 420 425 430
 Gly Phe Lys Lys Val Ala Asp Ala Met Leu Ala Gln Gly Val Ile
 435 440 445

50 <210> 83

<211> 20

<212> DNA

55 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for
amplifying gltA gene

<220>

<221> misc_feature

<222> (9)

<223> n=inosine

<400> 83

aagatcacnt acaatcgaygg

20

<210> 84

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for
amplifying gltA gene

<400> 84

tagaagtcta cgltcgggta

20

<210> 85

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for
amplifying gltA gene

<400> 85

gtcgacaata, gccatgaatct g

21

<210> 86

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for
amplifying gltA gene

<400> 86

cggtaggaacc ggtagcagaca t

21

<210> 87

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for
amplifying gltA gene

<400> 87

gggtgggga attcggtagc t

21

<210> 88

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for
amplifying gltA gene

<400> 88

tgtagcagacc gcgtagcgc a

21

<210> 89

<211> 1293

<212> DNA

<213> Corynebacterium thermoaminogenes

<220>

<221> CDS

<222> (1).. (1290)

<400> 89

| | | |
|----|---|-----|
| 5 | gfg gcl lcl gal aac aac aag gcl gla clg cac tac ccl ggc ggc gaa | 48 |
| | Val Ala Ser Asp Asn Asn Lys Ala Val Leu His Tyr Pro Gly Gly Glu | |
| | 1 5 10 15 | |
| | ttc gag atg ggc atc aag cag gcc acc gag ggt aac tcc ggt gtc atc | 96 |
| 10 | Phe Glu Met Gly Ile Lys Gln Ala Thr Glu Gly Asn Ser Gly Val Ile | |
| | 20 25 30 | |
| | ctg ggt aag atg ctg tgc gaa acc ggt ctg gtc acc ttc gac ccc ggt | 144 |
| | Leu Gly Lys Met Leu Ser Glu Thr Gly Leu Val Thr Phe Asp Pro Gly | |
| | 35 40 45 | |
| 15 | tat gtc agc acc ggt tcc acc gaa tcc aag atc acc tac atc gat ggt | 192 |
| | Tyr Val Ser Thr Gly Ser Thr Glu Ser Lys Ile Thr Tyr Ile Asp Gly | |
| | 50 55 60 | |
| 20 | gat gca ggc atc ctg cgc tac cgc ggc tac gac att gcg gat ctg gcc | 240 |
| | Asp Ala Gly Ile Leu Arg Tyr Arg Gly Tyr Asp Ile Ala Asp Leu Ala | |
| | 65 70 75 80 | |
| | gaa aat gcc acc ttc aat gag gtc tcc tac ctg atc aag ggt gag | 288 |
| 25 | Glu Asn Ala Thr Phe Asn Glu Val Ser Tyr Leu Leu Ile Lys Gly Glu | |
| | 85 90 95 | |
| | ctc ccg acc ccg gaa gag ctg cac aag ttc aac gac gag att cgt cac | 336 |
| | Leu Pro Thr Pro Glu Glu Leu His Lys Phe Asn Asp Glu Ile Arg His | |
| | 100 105 110 | |
| 30 | cac acc ctg ctg gac gag gac ttc aag tcc cag ttc aat gtc ttc cct | 384 |
| | His Thr Leu Leu Asp Glu Asp Phe Lys Ser Gln Phe Asn Val Phe Pro | |
| | 115 120 125 | |
| 35 | cgc gat gcc cac ccg atg gcc acc ctg gcc tcc tgc ggt aac atc ctg | 432 |
| | Arg Asp Ala His Pro Met Ala Thr Leu Ala Ser Ser Val Asn Ile Leu | |
| | 130 135 140 | |
| 40 | tcc acc tac tac cag gat cag ctg gat ccc ctg gat gag gct cag ctg | 480 |
| | Ser Thr Tyr Tyr Gln Asp Gln Leu Asp Pro Leu Asp Glu Ala Gln Leu | |
| | 145 150 155 160 | |
| | gac aag gca acc gtc cgc ctg atg gcg aag gtt ccg atg ctg gct gca | 528 |
| 45 | Asp Lys Ala Thr Val Arg Leu Met Ala Lys Val Pro Met Leu Ala Ala | |
| | 165 170 175 | |
| | tac gca cac cgt gcc cgc aag ggt gcg ccg tac atg tac ccg gac aac | 576 |
| | Tyr Ala His Arg Ala Arg Lys Gly Ala Pro Tyr Met Tyr Pro Asp Asn | |
| | 180 185 190 | |
| 50 | tcc ctg aat gcc cgt gag aac ttc ctg cgc atg atg ttc ggt tac ccg | 624 |
| | Ser Leu Asn Ala Arg Glu Asn Phe Leu Arg Met Met Phe Gly Tyr Pro | |
| | 195 200 205 | |
| 55 | acc gag ccg tac gag gtt gat ccg atc atg gtc aaa gcc ctg gac aag | 672 |
| | Thr Glu Pro Tyr Glu Val Asp Pro Ile Met Val Lys Ala Leu Asp Lys | |

210 215 220
 5 ctc ctc atc ctg cac gca gac cac gag cag aac tgc tcc acc tcc act 720
 Leu Leu Ile Leu His Ala Asp His Glu Gln Asn Cys Ser Thr Ser Thr
 225 230 235 240
 10 gtc cgc atg atc ggc tcc gcg cag gcg aac atg ttc gtc tcc atc gcc 768
 Val Arg Met Ile Gly Ser Ala Gln Ala Asn Met Phe Val Ser Ile Ala
 245 250 255
 ggc ggc atc aac gca ctc tcc ggc cgc ctg cac ggt ggc gcc aac cag 816
 Gly Gly Ile Asn Ala Leu Ser Gly Pro Leu His Gly Gly Ala Asn Gln
 260 265 270
 15 gct gtc ctc gag atg ctc gag gag atc gca gcc aac ggc ggc gac gca 864
 Ala Val Leu Glu Met Leu Glu Glu Ile Ala Ala Asn Gly Gly Asp Ala
 275 280 285
 20 acc gac ttc atg aac cgc gtc aag aac aag gag aag ggt gtc cgc ctc 912
 Thr Asp Phe Met Asn Arg Val Lys Asn Lys Glu Lys Gly Val Arg Leu
 290 295 300
 atg ggc ttc gga cac cgc gtc tac aag aac tac gat cgc cgt gca gcc 960
 Met Gly Phe Gly His Arg Val Tyr Lys Asn Tyr Asp Pro Arg Ala Ala
 305 310 315 320
 25 atc gtc aag gac acc gcc cac gag atc ctc gag cac ctc ggt ggc gac 1008
 Ile Val Lys Asp Thr Ala His Glu Ile Leu Glu His Leu Gly Gly Asp
 325 330 335
 30 cca ctg ctg gat ctg gct ctc aag ctg gaa gaa atc gca ctc aac gac 1056
 Pro Leu Leu Asp Leu Ala Leu Lys Leu Glu Glu Ile Ala Leu Asn Asp
 340 345 350
 35 gat tac ttc atc tcc cgc aag ctg tac ccg aac gtc gac ttc tac acc 1104
 Asp Tyr Phe Ile Ser Arg Lys Leu Tyr Pro Asn Val Asp Phe Tyr Thr
 355 360 365
 ggc ctg atc tac cgc gcc atg ggc ttc ccg acg gac ttc ttc acc gtc 1152
 Gly Leu Ile Tyr Arg Ala Met Gly Phe Pro Thr Asp Phe Phe Thr Val
 370 375 380
 40 ~~ctg ttc gcc atc ggc cgc ctc ccg ggc tgg atc gcc cac tac cgc gag~~ 1200
 Leu Phe Ala Ile Gly Arg Leu Pro Gly Trp Ile Ala His Tyr Arg Glu
 385 390 395 400
 45 cag ctc gcc gat ccg ggc gcc aag atc aac cgt cct cgc cag atc tac 1248
 Gln Leu Ala Asp Pro Gly Ala Lys Ile Asn Arg Pro Arg Gln Ile Tyr
 405 410 415
 50 acc ggt gag acc gca cgc aag atc atc ccc cgc gaa gag cgc tag 1293
 Thr Gly Glu Thr Ala Arg Lys Ile Ile Pro Arg Glu Glu Arg
 420 425 430
 55 <210> 90
 <211> 430

<212> PRT

<213> *Corynebacterium thermoaminogenes*

<400> 90

Val Ala Ser Asp Asn Asn Lys Ala Val Leu His Tyr Pro Gly Gly Glu
 1 5 10 15
 Phe Glu Met Gly Ile Lys Gln Ala Thr Glu Gly Asn Ser Gly Val Ile
 20 25 30
 Leu Gly Lys Met Leu Ser Glu Thr Gly Leu Val Thr Phe Asp Pro Gly
 35 40 45
 Tyr Val Ser Thr Gly Ser Thr Glu Ser Lys Ile Thr Tyr Ile Asp Gly
 50 55 60
 Asp Ala Gly Ile Leu Arg Tyr Arg Gly Tyr Asp Ile Ala Asp Leu Ala
 65 70 75 80
 Glu Asn Ala Thr Phe Asn Glu Val Ser Tyr Leu Leu Ile Lys Gly Glu
 85 90 95
 Leu Pro Thr Pro Glu Glu Leu His Lys Phe Asn Asp Glu Ile Arg His
 100 105 110
 His Thr Leu Leu Asp Glu Asp Phe Lys Ser Gln Phe Asn Val Phe Pro
 115 120 125
 Arg Asp Ala His Pro Met Ala Thr Leu Ala Ser Ser Val Asn Ile Leu
 130 135 140
 Ser Thr Tyr Tyr Gln Asp Gln Leu Asp Pro Leu Asp Glu Ala Gln Leu
 145 150 155 160
 Asp Lys Ala Thr Val Arg Leu Met Ala Lys Val Pro Met Leu Ala Ala
 165 170 175
 Tyr Ala His Arg Ala Arg Lys Gly Ala Pro Tyr Met Tyr Pro Asp Asn
 180 185 190
 Ser Leu Asn Ala Arg Glu Asn Phe Leu Arg Met Met Phe Gly Tyr Pro
 195 200 205
 Thr Glu Pro Tyr Glu Val Asp Pro Ile Met Val Lys Ala Leu Asp Lys
 210 215 220
 Leu Leu Ile Leu His Ala Asp His Glu Gln Asn Cys Ser Thr Ser Thr
 225 230 235 240
 Val Arg Met Ile Gly Ser Ala Gln Ala Asn Met Phe Val Ser Ile Ala
 245 250 255
 Gly Gly Ile Asn Ala Leu Ser Gly Pro Leu His Gly Gly Ala Asn Gln
 260 265 270
 Ala Val Leu Glu Met Leu Glu Glu Ile Ala Ala Asn Gly Gly Asp Ala
 275 280 285
 Thr Asp Phe Met Asn Arg Val Lys Asn Lys Glu Lys Gly Val Arg Leu
 290 295 300
 Met Gly Phe Gly His Arg Val Tyr Lys Asn Tyr Asp Pro Arg Ala Ala

305 310 315 320
 Ile Val Lys Asp Thr Ala His Glu Ile Leu Glu His Leu Gly Gly Asp
 325 330 335
 5 Pro Leu Leu Asp Leu Ala Leu Lys Leu Glu Glu Ile Ala Leu Asn Asp
 340 345 350
 Asp Tyr Phe Ile Ser Arg Lys Leu Tyr Pro Asn Val Asp Phe Tyr Thr
 355 360 365
 10 Gly Leu Ile Tyr Arg Ala Met Gly Phe Pro Thr Asp Phe Phe Thr Val
 370 375 380
 Leu Phe Ala Ile Gly Arg Leu Pro Gly Trp Ile Ala His Tyr Arg Glu
 385 390 395 400
 15 Gln Leu Ala Asp Pro Gly Ala Lys Ile Asn Arg Pro Arg Gln Ile Tyr
 405 410 415
 Thr Gly Glu Thr Ala Arg Lys Ile Ile Pro Arg Glu Glu Arg
 420 425 430
 20

<210> 91

<211> 1314

<212> DNA

<213> Brevibacterium lactofermentum

<220>

<221> CDS

<222> (1)..(1311)

<400> 91

35 atg ttt gaa agg gat atc gtg gct act gat aac aac aag gct gtc ctg 48
 Met Phe Glu Arg Asp Ile Val Ala Thr Asp Asn Asn Lys Ala Val Leu
 1 5 10 15
 40 cac tac ccc ggt ggc gag ttc gaa atg gac atc atc gag gct tct gag 96
 His Tyr Pro Gly Gly Glu Phe Glu Met Asp Ile Ile Glu Ala Ser Glu
 20 25 30

45 ggt aac aac ggt gtt gtc ctg ggc aag atg ctg tct gag act gga ctg 144
 Gly Asn Asn Gly Val Val Leu Gly Lys Met Leu Ser Glu Thr Gly Leu
 35 40 45
 50 atc act ttt gac cca ggt tat gtg agc act ggc tcc acc gag tcc aag 192
 Ile Thr Phe Asp Pro Gly Tyr Val Ser Thr Gly Ser Thr Glu Ser Lys
 50 55 60
 55 atc acc tac atc gat ggc gat ggc gga atc ctg cgt tac cgc ggc tat 240
 Ile Thr Tyr Ile Asp Gly Asp Ala Gly Ile Leu Arg Tyr Arg Gly Tyr
 65 70 75 80
 60 gac atc gct gat ctg gct gag aat gcc acc ttc aac gag gtt tct tac 288
 Asp Ile Ala Asp Leu Ala Glu Asn Ala Thr Phe Asn Glu Val Ser Tyr

EP 1 219 712 A1

| | | | | | | | |
|----|--|---|-----|----|--|----|--|
| | | 85 | | 90 | | 95 | |
| | | cla ctt atc aac ggt gaa cta cca acc cca gat gag ctt cac aag ttt | 336 | | | | |
| 5 | | Leu Leu Ile Asn Gly Glu Leu Pro Thr Pro Asp Glu Leu His Lys Phe | | | | | |
| | | 100 105 110 | | | | | |
| | | aac gac gag att cgc cac cac acc ctt ctg gag gag gac ttc aag tcc | 384 | | | | |
| | | Asn Asp Glu Ile Arg His His Thr Leu Leu Asp Glu Asp Phe Lys Ser | | | | | |
| 10 | | 115 120 125 | | | | | |
| | | cag ttc aac gtg ttc cca cgc gac gct cac cca atg gca acc ttg gct | 432 | | | | |
| | | Gln Phe Asn Val Phe Pro Arg Asp Ala His Pro Met Ala Thr Leu Ala | | | | | |
| | | 130 135 140 | | | | | |
| 15 | | ttc tct gtt aac att ttg tct acc tac tac cag gat cag ctg aac cca | 480 | | | | |
| | | Ser Ser Val Asn Ile Leu Ser Thr Tyr Tyr Gln Asp Gln Leu Asn Pro | | | | | |
| | | 145 150 155 160 | | | | | |
| | | ctc gat gag gca cag ctt gat aag gca acc gtt cgc ctc atg gca aag | 528 | | | | |
| 20 | | Leu Asp Glu Ala Gln Leu Asp Lys Ala Thr Val Arg Leu Met Ala Lys | | | | | |
| | | 165 170 175 | | | | | |
| | | gtt cca atg ctg gct gcg tac gca cac cgc gca cgc aag ggt gct cct | 576 | | | | |
| | | Val Pro Met Leu Ala Ala Tyr Ala His Arg Ala Arg Lys Gly Ala Pro | | | | | |
| 25 | | 180 185 190 | | | | | |
| | | tac atg tac cca gac aac tcc ctc aac gcg cgt gag aac ttc ctg cgc | 624 | | | | |
| | | Tyr Met Tyr Pro Asp Asn Ser Leu Asn Ala Arg Glu Asn Phe Leu Arg | | | | | |
| | | 195 200 205 | | | | | |
| 30 | | atg atg ttc ggt tac cca acc gag cca tac gag atc gac cca atc atg | 672 | | | | |
| | | Met Met Phe Gly Tyr Pro Thr Glu Pro Tyr Glu Ile Asp Pro Ile Met | | | | | |
| | | 210 215 220 | | | | | |
| 35 | | gtc aag gct ctg gac aag ctg ctc atc ctg cac gct gac cac gag cag | 720 | | | | |
| | | Val Lys Ala Leu Asp Lys Leu Leu Ile Leu His Ala Asp His Glu Gln | | | | | |
| | | 225 230 235 240 | | | | | |
| | | aac tgc tcc acc tcc acc gtt cgt atg atc ggt tcc gca cag gcc aac | 768 | | | | |
| 40 | | Asn Cys Ser Thr Ser Thr Val Arg Met Ile Gly Ser Ala Gln Ala Asn | | | | | |
| | | 245 250 255 | | | | | |
| | | atg ttt gtc tcc atc gct ggt ggc atc aac gct ctg tcc ggc cca ctg | 816 | | | | |
| | | Met Phe Val Ser Ile Ala Gly Gly Ile Asn Ala Leu Ser Gly Pro Leu | | | | | |
| | | 260 265 270 | | | | | |
| 45 | | cac ggt ggc gca aac cag gct gtt ctg gag atg ctc gaa gac atc aag | 864 | | | | |
| | | His Gly Gly Ala Asn Gln Ala Val Leu Glu Met Leu Glu Asp Ile Lys | | | | | |
| | | 275 280 285 | | | | | |
| 50 | | aac aac cac ggt ggc gac gca acc gcg ttc atg aac aag gtc aag aac | 912 | | | | |
| | | Asn Asn His Gly Gly Asp Ala Thr Ala Phe Met Asn Lys Val Lys Asn | | | | | |
| | | 290 295 300 | | | | | |
| | | aag gaa gac ggc gtc cgc ctc atg ggc ttc gga cac cgc gtt tac aag | 960 | | | | |
| | | Lys Glu Asp Gly Val Arg Leu Met Gly Phe Gly His Arg Val Tyr Lys | | | | | |
| 55 | | 305 310 315 320 | | | | | |

aac tac gal cca cgt gca gca atc gtc aag gag acc gca cac gag atc 1008
 Asn Tyr Asp Pro Arg Ala Ala Ile Val Lys Glu Thr Ala His Glu Ile
 325 330 335
 5 ctc gag cac ctc ggt ggc gac gal ctt ctg gal ctg gca atc aag ctg 1056
 Leu Glu His Leu Gly Gly Asp Asp Leu Leu Asp Leu Ala Ile Lys Leu
 340 345 350
 10 gaa gaa att gca ctg gct gal gal tac ttc atc tcc cgc aag ctc tac 1104
 Glu Glu Ile Ala Leu Ala Asp Asp Tyr Phe Ile Ser Arg Lys Leu Tyr
 355 360 365
 15 ccg aac gla gac ttc tac acc ggc ctg atc tac cgc gca atg ggc ttc 1152
 Pro Asn Val Asp Phe Tyr Thr Gly Leu Ile Tyr Arg Ala Met Gly Phe
 370 375 380
 cca act gac ttc ttc acc gla ttg ttc gca atc ggt cgt ctg cca gga 1200
 Pro Thr Asp Phe Phe Thr Val Leu Phe Ala Ile Gly Arg Leu Pro Gly
 385 390 395 400
 20 tgg atc gct cac tac cgc gag cag ctc ggt gca gca ggc aac aag atc 1248
 Trp Ile Ala His Tyr Arg Glu Gln Leu Gly Ala Ala Gly Asn Lys Ile
 405 410 415
 25 aac cgc cca cgc cag gtc tac acc ggc aag gaa tcc cgc aag ttg gtt 1296
 Asn Arg Pro Arg Gln Val Tyr Thr Gly Lys Glu Ser Arg Lys Leu Val
 420 425 430
 cct cgc gag gag cgc taa 1314
 30 Pro Arg Glu Glu Arg
 435

<210> 92

<211> 437

<212> PRT

<213> Brevibacterium lactofermentum

<400> 92

Met Phe Glu Arg Asp Ile Val Ala Thr Asp Asn Asn Lys Ala Val Leu

1 5 10 15
 45 His Tyr Pro Gly Gly Glu Phe Glu Met Asp Ile Ile Glu Ala Ser Glu
 20 25 30
 Gly Asn Asn Gly Val Val Leu Gly Lys Met Leu Ser Glu Thr Gly Leu
 35 40 45
 50 Ile Thr Phe Asp Pro Gly Tyr Val Ser Thr Gly Ser Thr Glu Ser Lys
 50 55 60
 Ile Thr Tyr Ile Asp Gly Asp Ala Gly Ile Leu Arg Tyr Arg Gly Tyr
 65 70 75 80
 55 Asp Ile Ala Asp Leu Ala Glu Asn Ala Thr Phe Asn Glu Val Ser Tyr
 85 90 95

| | | | | | | | | | | | | | | | | | |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| | Leu | Leu | Ile | Asn | Gly | Glu | Leu | Pro | Thr | Pro | Asp | Glu | Leu | His | Lys | Phe | |
| | | | | 100 | | | | | 105 | | | | | 110 | | | |
| 5 | Asn | Asp | Glu | Ile | Arg | His | His | Thr | Leu | Leu | Asp | Glu | Asp | Phe | Lys | Ser | |
| | | | 115 | | | | | 120 | | | | | 125 | | | | |
| | Gln | Phe | Asn | Val | Phe | Pro | Arg | Asp | Ala | His | Pro | Met | Ala | Thr | Leu | Ala | |
| | | | 130 | | | | 135 | | | | | 140 | | | | | |
| 10 | Ser | Ser | Val | Asn | Ile | Leu | Ser | Thr | Tyr | Tyr | Gln | Asp | Gln | Leu | Asn | Pro | |
| | 145 | | | | | 150 | | | | | 155 | | | | | 160 | |
| | Leu | Asp | Glu | Ala | Gln | Leu | Asp | Lys | Ala | Thr | Val | Arg | Leu | Met | Ala | Lys | |
| | | | | | 165 | | | | | 170 | | | | | 175 | | |
| 15 | Val | Pro | Met | Leu | Ala | Ala | Tyr | Ala | His | Arg | Ala | Arg | Lys | Gly | Ala | Pro | |
| | | | 180 | | | | | 185 | | | | | | 190 | | | |
| | Tyr | Met | Tyr | Pro | Asp | Asn | Ser | Leu | Asn | Ala | Arg | Glu | Asn | Phe | Leu | Arg | |
| | | 195 | | | | | 200 | | | | | | 205 | | | | |
| 20 | Met | Met | Phe | Gly | Tyr | Pro | Thr | Glu | Pro | Tyr | Glu | Ile | Asp | Pro | Ile | Met | |
| | | 210 | | | | | 215 | | | | | 220 | | | | | |
| | Val | Lys | Ala | Leu | Asp | Lys | Leu | Leu | Ile | Leu | His | Ala | Asp | His | Glu | Gln | |
| | 225 | | | | | 230 | | | | | 235 | | | | | 240 | |
| 25 | Asn | Cys | Ser | Thr | Ser | Thr | Val | Arg | Met | Ile | Gly | Ser | Ala | Gln | Ala | Asn | |
| | | | | 245 | | | | | | 250 | | | | | 255 | | |
| | Met | Phe | Val | Ser | Ile | Ala | Gly | Gly | Ile | Asn | Ala | Leu | Ser | Gly | Pro | Leu | |
| | | | 260 | | | | | 265 | | | | | 270 | | | | |
| 30 | His | Gly | Gly | Ala | Asn | Gln | Ala | Val | Leu | Glu | Met | Leu | Glu | Asp | Ile | Lys | |
| | | 275 | | | | | | 280 | | | | | 285 | | | | |
| | Asn | Asn | His | Gly | Gly | Asp | Ala | Thr | Ala | Phe | Met | Asn | Lys | Val | Lys | Asn | |
| | | 290 | | | | | 295 | | | | | 300 | | | | | |
| 35 | Lys | Glu | Asp | Gly | Val | Arg | Leu | Met | Gly | Phe | Gly | His | Arg | Val | Tyr | Lys | |
| | 305 | | | | | 310 | | | | | 315 | | | | | 320 | |
| | Asn | Tyr | Asp | Pro | Arg | Ala | Ala | Ile | Val | Lys | Glu | Thr | Ala | His | Glu | Ile | |
| | | | | | 325 | | | | | 330 | | | | | 335 | | |
| 40 | Leu | Glu | His | Leu | Gly | Gly | Asp | Asp | Leu | Leu | Asp | Leu | Ala | Ile | Lys | Leu | |
| | | | 340 | | | | | | 345 | | | | | 350 | | | |
| | Glu | Glu | Ile | Ala | Leu | Ala | Asp | Asp | Tyr | Phe | Ile | Ser | Arg | Lys | Leu | Tyr | |
| | | 355 | | | | | | 360 | | | | | 365 | | | | |
| 45 | Pro | Asn | Val | Asp | Phe | Tyr | Thr | Gly | Leu | Ile | Tyr | Arg | Ala | Met | Gly | Phe | |
| | | 370 | | | | | 375 | | | | | 380 | | | | | |
| | Pro | Thr | Asp | Phe | Phe | Thr | Val | Leu | Phe | Ala | Ile | Gly | Arg | Leu | Pro | Gly | |
| | 385 | | | | | 390 | | | | | 395 | | | | | 400 | |
| 50 | Trp | Ile | Ala | His | Tyr | Arg | Glu | Gln | Leu | Gly | Ala | Ala | Gly | Asn | Lys | Ile | |
| | | | | 405 | | | | | | 410 | | | | | 415 | | |
| | Asn | Arg | Pro | Arg | Gln | Val | Tyr | Thr | Gly | Lys | Glu | Ser | Arg | Lys | Leu | Val | |
| | | | | 420 | | | | | 425 | | | | | 430 | | | |
| 55 | Pro | Arg | Glu | Glu | Arg | | | | | | | | | | | | |

435

<210> 93

<211> 1656

<212> DNA

<213> Corynebacterium thermoaminogenes

<220>

<221> CDS

<222> (309).. (1595)

<400> 93

```

acgcccgatt ctccaacact atcgaagagg tcccaaccca cgcgttgacc cagggcctgg 60
gtactttgtc ccgcgcgcaa aatacgtgt tggiggcaac tggccaagga aaagcagaca 120
gccatccgcg gaactgigga aggtccagtg actgcttcit gcccagggtc cattctgcaa 180
atgcacaaca acgccacat cactgtgat gaagcagcag calccaagct gaaaaatgct 240
gaccattacc gctcatgga gcaattaaag ctgcgctaga aacaaaaagg aaagtacgtg 300
gtggggct atg cac aca gaa ctt tcc agt ttg cgc cct gcg tac cat gtg 350
Met His Thr Glu Leu Ser Ser Leu Arg Pro Ala Tyr His Val
      1           5           10
act cct ccg cag ggc aga ctc aat gat ccc aat gga atg tac gtc gat 398
Thr Pro Pro Gln Gly Arg Leu Asn Asp Pro Asn Gly Met Tyr Val Asp
      15           20           25           30
gga gat acc ctc cac gtc tac tac cag cac gat cca ggt ttc ccc ttc 446
Gly Asp Thr Leu His Val Tyr Tyr Gln His Asp Pro Gly Phe Pro Phe
      35           40           45
gca cca aag cgc acc ggt tgg gct cac acc acc acg ccg ttg acc gga 494
Ala Pro Lys Arg Thr Gly Trp Ala His Thr Thr Thr Pro Leu Thr Gly
      50           55           60
ccg cag cga ttg cag tgg acg cac ctg ccc gat gct ctt tac ccg gat 542
Pro Gln Arg Leu Gln Trp Thr His Leu Pro Asp Ala Leu Tyr Pro Asp
      65           70           75
gta tcc tat gac ctg gat gga tgc tat tcc ggc gga gcc gta ttt tct 590
Val Ser Tyr Asp Leu Asp Gly Cys Tyr Ser Gly Gly Ala Val Phe Ser
      80           85           90
gac ggc acg ctt aaa ctt ttc tac acc ggc aac cga aaa att gac ggc 638
Asp Gly Thr Leu Lys Leu Phe Tyr Thr Gly Asn Arg Lys Ile Asp Gly
      95           100           105           110
aag cgc cgc gcc acc caa aac ctc gtc gaa gtc gag gac cca act ggc 686
Lys Arg Arg Ala Thr Gln Asn Leu Val Glu Val Glu Asp Pro Thr Gly
      115           120           125
ctg atg ggc ggc att cat cgc cgc tgc cct aaa aat ccg ctt atc gac 734
Leu Met Gly Gly Ile His Arg Arg Ser Pro Lys Asn Pro Leu Ile Asp

```

| | | | | |
|----|---|------|-----|-----|
| | 130 | 135 | 140 | |
| | gga ccc gcc agc ggt ttt acg ccc cac tac cgc gat ccc atg atc agc | 782 | | |
| 5 | Gly Pro Ala Ser Gly Phe Thr Pro His Tyr Arg Asp Pro Met Ile Ser | | | |
| | 145 | 150 | 155 | |
| | cct gat ggg gat ggt tgg aag atg gtt ctt ggg gct cag cgc gaa aac | 830 | | |
| | Pro Asp Gly Asp Gly Trp Lys Met Val Leu Gly Ala Gln Arg Glu Asn | | | |
| 10 | 160 | 165 | 170 | |
| | ctc acc ggt gca gcg gtt cta tac cgc tcg gca gat ctt gaa aac tgg | 878 | | |
| | Leu Thr Gly Ala Ala Val Leu Tyr Arg Ser Ala Asp Leu Glu Asn Trp | | | |
| | 175 | 180 | 185 | 190 |
| 15 | gaa ttc tcc ggt gaa atc acc ttt gac ctc agc gac gca caa cct ggt | 926 | | |
| | Glu Phe Ser Gly Glu Ile Thr Phe Asp Leu Ser Asp Ala Gln Pro Gly | | | |
| | 195 | 200 | 205 | |
| 20 | tct gcc cct gat ctc gtt cct ggc ggc tac atg tgg gaa tgc ccc aac | 974 | | |
| | Ser Ala Pro Asp Leu Val Pro Gly Gly Tyr Met Trp Glu Cys Pro Asn | | | |
| | 210 | 215 | 220 | |
| | ctt ttt acg ctt cgc gat gaa aaa acc ggc gaa gac ctc gat gtg ctg | 1022 | | |
| | Leu Phe Thr Leu Arg Asp Glu Lys Thr Gly Glu Asp Leu Asp Val Leu | | | |
| 25 | 225 | 230 | 235 | |
| | att ttc tgt cca caa gga ttg gac cgt atc gat gat gag gtt act cac | 1070 | | |
| | Ile Phe Cys Pro Gln Gly Leu Asp Arg Ile Asp Asp Glu Val Thr His | | | |
| | 240 | 245 | 250 | |
| 30 | tac gca agc tct gac cag tgc gga tat gtc gtc ggc aag ctt gaa gaa | 1118 | | |
| | Tyr Ala Ser Ser Asp Gln Cys Gly Tyr Val Val Gly Lys Leu Glu Glu | | | |
| | 255 | 260 | 265 | 270 |
| 35 | acg acc ttc cgt gtc ctg cga gga ttc agc gag ctg gat ttc ggt cat | 1166 | | |
| | Thr Thr Phe Arg Val Leu Arg Gly Phe Ser Glu Leu Asp Phe Gly His | | | |
| | 275 | 280 | 285 | |
| | gaa ttc tac gcg ccg cag gtt gca gtc aac ggt tcc gat gcc tgg ctt | 1214 | | |
| | Glu Phe Tyr Ala Pro Gln Val Ala Val Asn Gly Ser Asp Ala Trp Leu | | | |
| 40 | 290 | 295 | 300 | |
| | gtg ggc tgg atg gga ttg cct gca cag gat gat cac cca aca gtt gcg | 1262 | | |
| | Val Gly Trp Met Gly Leu Pro Ala Gln Asp Asp His Pro Thr Val Ala | | | |
| | 305 | 310 | 315 | |
| 45 | cag gaa gga tgg gtg cac tgc ctg acc gtt cct cgc agg ctt cat ttg | 1310 | | |
| | Gln Glu Gly Trp Val His Cys Leu Thr Val Pro Arg Arg Leu His Leu | | | |
| | 320 | 325 | 330 | |
| 50 | cgt aac cat gcg atc tat caa gag ctt ctt ctc cca gaa ggg gag tgc | 1358 | | |
| | Arg Asn His Ala Ile Tyr Gln Glu Leu Leu Leu Pro Glu Gly Glu Ser | | | |
| | 335 | 340 | 345 | 350 |
| | ggg gta act aga tct gta tta ggt tct gaa cct gtc cga gta gac atc | 1406 | | |
| | Gly Val Thr Arg Ser Val Leu Gly Ser Glu Pro Val Arg Val Asp Ile | | | |
| 55 | 355 | 360 | 365 | |

EP 1219712 A1

cga gac aat gtt tcc ctc gag tgg gat ggt gtc cgg ttg tct gtg gat 1454
 Arg Asp Asn Val Ser Leu Glu Trp Asp Gly Val Arg Leu Ser Val Asp
 370 375 380
 5 cgc gat ggc gat cgt cgt gla gct gaa gla aaa cct ggc gaa tta gtg 1502
 Arg Asp Gly Asp Arg Arg Val Ala Glu Val Lys Pro Gly Glu Leu Val
 385 390 395
 10 atc gcg gac gat aat aca gcg att gag ala aca gca ggt cat ggc cag 1550
 Ile Ala Asp Asp Asn Thr Ala Ile Glu Ile Thr Ala Gly His Gly Gln
 400 405 410
 gtt tcc ttc gct ttc cgc acc ttc aaa ggt gac act att gag aga 1595
 Val Ser Phe Ala Phe Arg Thr Phe Lys Gly Asp Thr Ile Glu Arg
 15 415 420 425
 taagtcataaa aaaaggccct tcgtggcggt atgtacaaa tacttcgcaa aatcccttga 1655
 t 1656
 20 <210> 94
 <211> 429
 <212> PRT
 25 <213> Corynebacterium thermoaminogenes
 <400> 94
 Met His Thr Glu Leu Ser Ser Leu Arg Pro Ala Tyr His Val Thr Pro
 30 1 5 10 15
 Pro Gln Gly Arg Leu Asn Asp Pro Asn Gly Met Tyr Val Asp Gly Asp
 20 25 30
 Thr Leu His Val Tyr Tyr Gln His Asp Pro Gly Phe Pro Phe Ala Pro
 35 35 40 45
 Lys Arg Thr Gly Trp Ala His Thr Thr Thr Pro Leu Thr Gly Pro Gln
 50 55 60
 Arg Leu Gln Trp Thr His Leu Pro Asp Ala Leu Tyr Pro Asp Val Ser
 40 65 70 75 80
 Tyr Asp Leu Asp Gly Cys Tyr Ser Gly Gly Ala Val Phe Ser Asp Gly
 85 90 95
 Thr Leu Lys Leu Phe Tyr Thr Gly Asn Arg Lys Ile Asp Gly Lys Arg
 45 100 105 110
 Arg Ala Thr Gln Asn Leu Val Glu Val Glu Asp Pro Thr Gly Leu Met
 115 120 125
 Gly Gly Ile His Arg Arg Ser Pro Lys Asn Pro Leu Ile Asp Gly Pro
 50 130 135 140
 Ala Ser Gly Phe Thr Pro His Tyr Arg Asp Pro Met Ile Ser Pro Asp
 145 150 155 160
 Gly Asp Gly Trp Lys Met Val Leu Gly Ala Gln Arg Glu Asn Leu Thr
 55 165 170 175

| | | | | | | | | | | | | | | | | |
|----|---|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| | Gly | Ala | Ala | Val | Leu | Tyr | Arg | Ser | Ala | Asp | Leu | Glu | Asn | Trp | Glu | Phe |
| | | | | 180 | | | | | 185 | | | | | 190 | | |
| 5 | Ser | Gly | Glu | Ile | Thr | Phe | Asp | Leu | Ser | Asp | Ala | Gln | Pro | Gly | Ser | Ala |
| | | | 195 | | | | | 200 | | | | | 205 | | | |
| | Pro | Asp | Leu | Val | Pro | Gly | Gly | Tyr | Met | Trp | Glu | Cys | Pro | Asn | Leu | Phe |
| | | 210 | | | | 215 | | | | | 220 | | | | | |
| 10 | Thr | Leu | Arg | Asp | Glu | Lys | Thr | Gly | Glu | Asp | Leu | Asp | Val | Leu | Ile | Phe |
| | 225 | | | | 230 | | | | | | 235 | | | | 240 | |
| | Cys | Pro | Gln | Gly | Leu | Asp | Arg | Ile | Asp | Asp | Glu | Val | Thr | His | Tyr | Ala |
| | | | | 245 | | | | | 250 | | | | | 255 | | |
| 15 | Ser | Ser | Asp | Gln | Cys | Gly | Tyr | Val | Val | Gly | Lys | Leu | Glu | Glu | Thr | Thr |
| | | | 260 | | | | | | 265 | | | | | 270 | | |
| | Phe | Arg | Val | Leu | Arg | Gly | Phe | Ser | Glu | Leu | Asp | Phe | Gly | His | Glu | Phe |
| | | 275 | | | | | | 280 | | | | | 285 | | | |
| 20 | Tyr | Ala | Pro | Gln | Val | Ala | Val | Asn | Gly | Ser | Asp | Ala | Trp | Leu | Val | Gly |
| | | 290 | | | | | 295 | | | | | 300 | | | | |
| | Trp | Met | Gly | Leu | Pro | Ala | Gln | Asp | Asp | His | Pro | Thr | Val | Ala | Gln | Glu |
| | 305 | | | | 310 | | | | | | 315 | | | | 320 | |
| 25 | Gly | Trp | Val | His | Cys | Leu | Thr | Val | Pro | Arg | Arg | Leu | His | Leu | Arg | Asn |
| | | | | 325 | | | | | 330 | | | | | 335 | | |
| | His | Ala | Ile | Tyr | Gln | Glu | Leu | Leu | Leu | Pro | Glu | Gly | Glu | Ser | Gly | Val |
| | | | 340 | | | | | | 345 | | | | | 350 | | |
| 30 | Thr | Arg | Ser | Val | Leu | Gly | Ser | Glu | Pro | Val | Arg | Val | Asp | Ile | Arg | Asp |
| | | 355 | | | | | | 360 | | | | | 365 | | | |
| | Asn | Val | Ser | Leu | Glu | Trp | Asp | Gly | Val | Arg | Leu | Ser | Val | Asp | Arg | Asp |
| | | 370 | | | | | 375 | | | | 380 | | | | | |
| 35 | Gly | Asp | Arg | Arg | Val | Ala | Glu | Val | Lys | Pro | Gly | Glu | Leu | Val | Ile | Ala |
| | 385 | | | | 390 | | | | | | 395 | | | | 400 | |
| | Asp | Asp | Asn | Thr | Ala | Ile | Glu | Ile | Thr | Ala | Gly | His | Gly | Gln | Val | Ser |
| | | | | 405 | | | | | 410 | | | | | 415 | | |
| 40 | Phe | Ala | Phe | Arg | Thr | Phe | Lys | Gly | Asp | Thr | Ile | Glu | Arg | | | |
| | | | 420 | | | | | 425 | | | | | | | | |
| 45 | <210> 95 | | | | | | | | | | | | | | | |
| | <211> 35 | | | | | | | | | | | | | | | |
| | <212> DNA | | | | | | | | | | | | | | | |
| 50 | <213> Artificial Sequence | | | | | | | | | | | | | | | |
| | <220> | | | | | | | | | | | | | | | |
| 55 | <223> Description of Artificial Sequence: primer for amplifying scrB gene | | | | | | | | | | | | | | | |

<400> 95
gtacataatg tcgttagaac gcgtaatacg actca

35

5 <210> 96
<211> 35
<212> DNA

10 <213> Artificial Sequence

<220>
15 <223> Description of Artificial Sequence:primer for
amplifying scrB gene

<400> 96
20 cgttagaacg cgtaatacga ctactatag ggaga

35

<210> 97
<211> 30
25 <212> DNA

<213> Artificial Sequence

30 <220>
<223> Description of Artificial Sequence:primer for
LA cloning of scrB

35 <400> 97
gtaaagagcg tggggcaggt gcgtccactg

30

<210> 98
40 <211> 30
<212> DNA

45 <213> Artificial Sequence

<220>
50 <223> Description of Artificial Sequence:primer for
LA cloning of scrB

<400> 98
gggtgagcc cagccggtag gcattggtag

30

55 <210> 99

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for
LA cloning of scrB

<400> 99

atcagccclg atggtaggg ttggaaaatg

30

<210> 100

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for
LA cloning of scrB gene

<400> 100

ggtagcagcgg ttctataccg ctgcacagat

30

<210> 101

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for
amplifying scrB gene

<400> 101

ggcccgggac gcccgattct tcaacactat cg

32

<210> 102

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer for
amplifying scrB gene

<400> 102

ggccccgggga tcaagggatt ttgcaagta tt

32

<210> 103

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer for
amplifying icd gene

<400> 103

gaagatctct atgaccagcg catcaagctg

30

<210> 104

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer for
amplifying icd gene

<400> 104

gaagatctgg tcatccaga accgatcac

30

<210> 105

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer for
amplifying gdh gene

<400> 105

gcgcctgcag gtccgagggg gtgcgttcgg ca

32

<210> 106

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for
amplifying gdh gene

<400> 106

gcgcctgcag gcaccaggat gccctcaacc ag

32

<210> 107

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for
amplifying gltA gene

<400> 107

ggggataccga tcactataac cccacagcac

30

<210> 108

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for
amplifying gltA gene

<400> 108

ggggatccct ggctgatctg aactaggcgc

30

Claims

1. A protein having the amino acid sequence of SEQ ID NO: 2 or the amino acid sequence of SEQ ID NO: 2 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, which has isocitrate lyase activity and shows 30% or more of residual activity after a heat treatment at 50°C for 5 minutes.
2. A protein having the amino acid sequence of SEQ ID NO: 4 or the amino acid sequence of SEQ ID NO: 4 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, which is involved in acyl Co-A carboxylase activity and is derived from *Corynebacterium thermoaminogenes*.
3. A protein having the amino acid sequence of SEQ ID NO: 6 or the amino acid sequence of SEQ ID NO: 6 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, which has DtsR activity and is derived from *Corynebacterium thermoaminogenes*.
4. A protein having the amino acid sequence of SEQ ID NO: 8 or the amino acid sequence of SEQ ID NO: 8 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, which has DtsR activity and is derived from *Corynebacterium thermoaminogenes*.
5. A protein having the amino acid sequence of SEQ ID NO: 10 or the amino acid sequence of SEQ ID NO: 10 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, which shows phosphofructokinase activity at 60°C in an equivalent or higher degree compared with the activity at 30°C.
6. A protein having the amino acid sequence of SEQ ID NO: 94 or the amino acid sequence of SEQ ID NO: 94 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, which has activity for imparting sucrose assimilating ability to *Corynebacterium thermoaminogenes*.
7. A protein having any one of the amino acid sequences of SEQ ID NOS: 17-20 or the amino acid sequence of any one of SEQ ID NOS: 17-20 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, which has a function involved in glutamic acid uptake and is derived from *Corynebacterium thermoaminogenes*.
8. A protein having the amino acid sequence of SEQ ID NO: 22 or the amino acid sequence of SEQ ID NO: 22 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, which has pyruvate dehydrogenase activity and is derived from *Corynebacterium thermoaminogenes*.
9. A protein having the amino acid sequence of SEQ ID NO: 24 or the amino acid sequence of SEQ ID NO: 24 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, which has pyruvate carboxylase activity and is derived from *Corynebacterium thermoaminogenes*.
10. A protein having the amino acid sequence of SEQ ID NO: 26 or the amino acid sequence of SEQ ID NO: 26 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, which has phosphoenolpyruvate carboxylase activity and shows 50% or more of residual activity after a heat treatment at 45°C for 5 minutes.
11. A protein having the amino acid sequence of SEQ ID NO: 28 or the amino acid sequence of SEQ ID NO: 28 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, which has aconitase activity and shows 30% or more of residual activity after a heat treatment at 50°C for 3 minutes.
12. A protein having the amino acid sequence of SEQ ID NO: 30 or the amino acid sequence of SEQ ID NO: 30 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, which has isocitrate dehydrogenase activity and shows 50% or more of residual activity after a heat treatment at 45°C for 10 minutes.
13. A protein having the amino acid sequence of SEQ ID NO: 32 or the amino acid sequence of SEQ ID NO: 32 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, which has dihydroipoamide dehydrogenase activity and is derived from *Corynebacterium thermoaminogenes*.
14. A protein having the amino acid sequence of SEQ ID NO: 34 or the amino acid sequence of SEQ ID NO: 34

including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, which has 2-oxoglutarate dehydrogenase activity and shows 30% or more of residual activity after a heat treatment at 50°C for 10 minutes.

- 5 15. A protein having the amino acid sequence of SEQ ID NO: 80 in Sequence Listing or the amino acid sequence of SEQ ID NO: 80 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, which shows glutamate dehydrogenase activity at 42°C in an equivalent or higher degree compared with the activity at 37°C.
- 10 16. A protein having the amino acid sequence of SEQ ID NO: 90 in Sequence Listing or the amino acid sequence of SEQ ID NO: 90 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, which shows citrate synthase activity at 37°C in an equivalent or higher degree compared with the activity at 23°C.
- 15 17. A DNA which codes for a protein having the amino acid sequence of SEQ ID NO: 2 or the amino acid sequence of SEQ ID NO: 2 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, and having isocitrate lyase activity.
- 20 18. The DNA according to Claim 17, which is a DNA defined in the following (a1) or (b1):
 - (a1) a DNA which comprises the nucleotide sequence of SEQ ID NO: 1 in Sequence Listing,
 - (b1) a DNA which is hybridizable with the nucleotide sequence of SEQ ID NO: 1 in Sequence Listing or a primer prepared based on the nucleotide sequence under a stringent condition, and codes for a protein having isocitrate lyase activity.
- 25 19. A DNA which codes for a protein having the amino acid sequence of SEQ ID NO: 4 or the amino acid sequence of SEQ ID NO: 4 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, and involved in acyl Co-A carboxylase activity.
- 30 20. The DNA according to Claim 19, which is a DNA defined in the following (a2) or (b2):
 - (a2) a DNA which comprises the nucleotide sequence of SEQ ID NO: 3 in Sequence Listing,
 - (b2) a DNA which is hybridizable with the nucleotide sequence of SEQ ID NO: 3 in Sequence Listing or a primer prepared based on the nucleotide sequence under a stringent condition, and codes for a protein involved in acyl Co-A carboxylase activity.
- 35 21. A DNA which codes for a protein having the amino acid sequence of SEQ ID NO: 6 or the amino acid sequence of SEQ ID NO: 6 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, and having DtsR activity.
- 40 22. The DNA according to Claim 21, which is a DNA defined in the following (a3) or (b3):
 - (a3) a DNA which comprises the nucleotide sequence of SEQ ID NO: 5 in Sequence Listing,
 - (b3) a DNA which is hybridizable with the nucleotide sequence of SEQ ID NO: 5 in Sequence Listing or a primer prepared based on the nucleotide sequence under a stringent condition, and codes for a protein having DtsR activity.
- 45 23. A DNA which codes for a protein having the amino acid sequence of SEQ ID NO: 8 or the amino acid sequence of SEQ ID NO: 8 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, and having DtsR activity.
- 50 24. The DNA according to Claim 23, which is a DNA defined in the following (a4) or (b4):
 - (a4) a DNA which comprises the nucleotide sequence of SEQ ID NO: 7 in Sequence Listing,
 - (b4) a DNA which is hybridizable with the nucleotide sequence of SEQ ID NO: 7 in Sequence Listing or a primer prepared based on the nucleotide sequence under a stringent condition, and codes for a protein having DtsR activity.
- 55

25. A DNA which codes for a protein having the amino acid sequence of SEQ ID NO: 10 or the amino acid sequence of SEQ ID NO: 10 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, and having phosphofructokinase activity.

5 26. The DNA according to Claim 25, which is a DNA defined in the following (a5) or (b5):

(a5) a DNA which comprises the nucleotide sequence of SEQ ID NO: 9 in Sequence Listing,

(b5) a DNA which is hybridizable with the nucleotide sequence of SEQ ID NO: 9 in Sequence Listing or a primer prepared based on the nucleotide sequence under a stringent condition, and codes for a protein having phosphofructokinase activity.

10

27. A DNA which codes for a protein having the amino acid sequence of SEQ ID NO: 93 or the amino acid sequence of SEQ ID NO: 93 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, and having invertase activity.

15

28. The DNA according to Claim 27, which is a DNA defined in the following (a6) or (b6):

(a6) a DNA which comprises the nucleotide sequence of SEQ ID NO: 93 in Sequence Listing,

(b6) a DNA which is hybridizable with the nucleotide sequence of SEQ ID NO: 93 in Sequence Listing or a primer prepared based on the nucleotide sequence under a stringent condition, and codes for a protein having invertase activity.

20

29. A DNA which codes for a protein having any one of the amino acid sequences of SEQ ID NOS: 17-20 or the amino acid sequence of any one of SEQ ID NOS: 17-20 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, and having a function involved in glutamic acid uptake.

25

30. The DNA according to Claim 29, which is a DNA defined in the following (a7) or (b7):

(a7) a DNA which comprises the nucleotide sequence of SEQ ID NO: 16 in Sequence Listing,

(b7) a DNA which is hybridizable with the nucleotide sequence of SEQ ID NO: 16 in Sequence Listing or a primer prepared based on the nucleotide sequence under a stringent condition, and codes for a protein having a function involved in glutamic acid uptake.

30

31. A DNA which codes for a protein having the amino acid sequence of SEQ ID NO: 22 or the amino acid sequence of SEQ ID NO: 22 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, and having pyruvate dehydrogenase activity.

35

32. The DNA according to Claim 31, which is a DNA defined in the following (a8) or (b8):

(a8) a DNA which comprises the nucleotide sequence of SEQ ID NO: 21 in Sequence Listing,

(b8) a DNA which is hybridizable with the nucleotide sequence of SEQ ID NO: 21 in Sequence Listing or a primer prepared based on the nucleotide sequence under a stringent condition, and codes for a protein having pyruvate dehydrogenase activity.

40

33. A DNA which codes for a protein having the amino acid sequence of SEQ ID NO: 24 or the amino acid sequence of SEQ ID NO: 24 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, and having pyruvate carboxylase activity.

45

34. A DNA according to Claim 33, which is a DNA defined in the following (a9) or (b9):

(a9) a DNA which comprises the nucleotide sequence of SEQ ID NO: 23 in Sequence Listing,

(b9) a DNA which is hybridizable with the nucleotide sequence of SEQ ID NO: 23 in Sequence Listing or a primer prepared based on the nucleotide sequence under a stringent condition, and codes for a protein having pyruvate carboxylase activity.

50

35. A DNA which codes for a protein having the amino acid sequence of SEQ ID NO: 26 or the amino acid sequence of SEQ ID NO: 26 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, and having phosphoenolpyruvate carboxylase activity.

55

36. The DNA according to Claim 35, which is a DNA defined in the following (a10) or (b10):

(a10) a DNA which comprises the nucleotide sequence of SEQ ID NO: 25 in Sequence Listing

(b10) a DNA which is hybridizable with the nucleotide sequence of SEQ ID NO: 25 in Sequence Listing or a primer prepared based on the nucleotide sequence under a stringent condition, and codes for a protein having phosphoenolpyruvate carboxylase activity.

37. A DNA which codes for a protein having the amino acid sequence of SEQ ID NO: 28 or the amino acid sequence of SEQ ID NO: 28 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, and having aconitase activity.

38. The DNA according to Claim 37, which is a DNA defined in the following (a11) or (b11):

(a11) a DNA which comprises the nucleotide sequence of SEQ ID NO: 27 in Sequence Listing.

(b11) a DNA which is hybridizable with the nucleotide sequence of SEQ ID NO: 27 in Sequence Listing or a primer prepared based on the nucleotide sequence under a stringent condition, and codes for a protein having aconitase activity.

39. A DNA which codes for a protein having the amino acid sequence of SEQ ID NO: 30 or the amino acid sequence of SEQ ID NO: 30 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, and having isocitrate dehydrogenase activity.

40. The DNA according to Claim 39, which is a DNA defined in the following (a12) or (b12):

(a12) a DNA which comprises the nucleotide sequence of SEQ ID NO: 27 in Sequence Listing.

(b12) a DNA which is hybridizable with the nucleotide sequence of SEQ ID NO: 27 in Sequence Listing or a primer prepared based on the nucleotide sequence under a stringent condition, and codes for a protein having isocitrate dehydrogenase activity.

41. A DNA which codes for a protein having the amino acid sequence of SEQ ID NO: 32 or the amino acid sequence of SEQ ID NO: 32 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, and having dihydrolipoamide dehydrogenase activity.

42. The DNA according to Claim 41, which is a DNA defined in the following (a13) or (b13):

(a13) a DNA which comprises the nucleotide sequence of SEQ ID NO: 31 in Sequence Listing.

(b13) a DNA which is hybridizable with the nucleotide sequence of SEQ ID NO: 31 in Sequence Listing or a primer prepared based on the nucleotide sequence under a stringent condition, and codes for a protein having dihydrolipoamide dehydrogenase activity.

43. A DNA which codes for a protein having the amino acid sequence of SEQ ID NO: 34 or the amino acid sequence of SEQ ID NO: 34 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, and having 2-oxoglutarate dehydrogenase activity.

44. The DNA according to Claim 43, which is a DNA defined in the following (a14) or (b14):

(a14) a DNA which comprises the nucleotide sequence of SEQ ID NO: 33 in Sequence Listing.

(b14) a DNA which is hybridizable with the nucleotide sequence of SEQ ID NO: 33 in Sequence Listing or a primer prepared based on the nucleotide sequence under a stringent condition, and codes for a protein having 2-oxoglutarate dehydrogenase activity.

45. A DNA which codes for a protein having the amino acid sequence of SEQ ID NO: 80 in Sequence Listing or the amino acid sequence of SEQ ID NO: 80 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, and showing glutamate dehydrogenase activity at 42°C in an equivalent or higher degree compared with the activity at 37°C.

46. The DNA according to Claim 45, which is a DNA defined in the following (a15) or (b15):

(a15) a DNA which comprises the nucleotide sequence of SEQ ID NO: 79 in Sequence Listing,

(b15) a DNA which is hybridizable with the nucleotide sequence of SEQ ID NO: 79 in Sequence Listing or a primer prepared based on the nucleotide sequence under a stringent condition, and codes for a protein showing glutamate dehydrogenase activity at 42°C in an equivalent or higher degree compared with the activity at 37°C.

5

47. A DNA which codes for a protein having the amino acid sequence of SEQ ID NO: 90 in Sequence Listing or the amino acid sequence of SEQ ID NO: 90 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, and showing citrate synthase activity at 37°C in an equivalent or higher degree compared with the activity at 23°C.

10

48. The DNA according to Claims 47, which is a DNA defined in the following (a16) or (b16):

(a16) a DNA which comprises the nucleotide sequence of SEQ ID NO: 89 in Sequence Listing,

(b16) a DNA which is hybridizable with the nucleotide sequence of SEQ ID NO: 89 in Sequence Listing or a primer prepared based on the nucleotide sequence under a stringent condition, and codes for a protein showing citrate synthase activity at 37°C in an equivalent or higher degree compared with the activity at 23°C.

15

49. A method for producing L-amino acid, which comprises culturing a microorganism introduced with a DNA according to any one of Claims 17 to 48 in a medium to produce and accumulate L-amino acid in the medium, and collecting the L-amino acid from the medium.

20

25

30

35

40

45

50

55

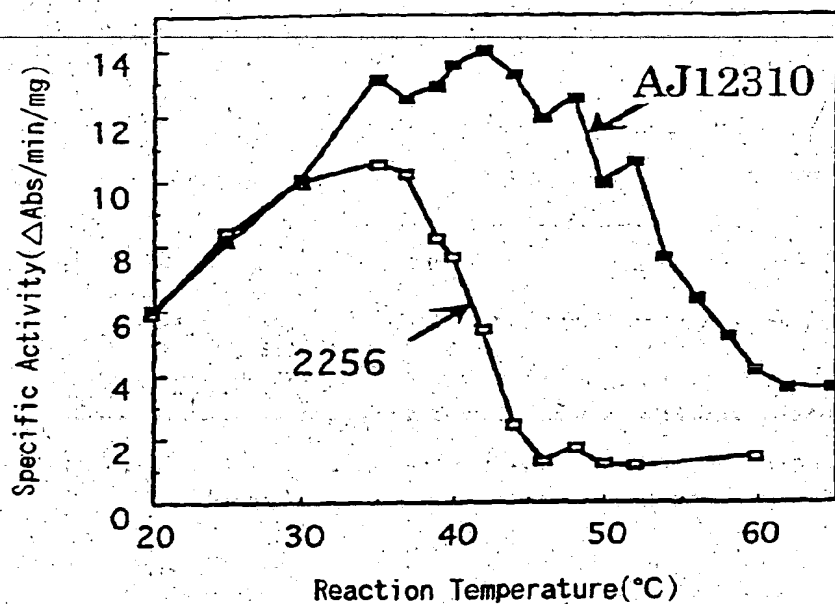


Fig. 1

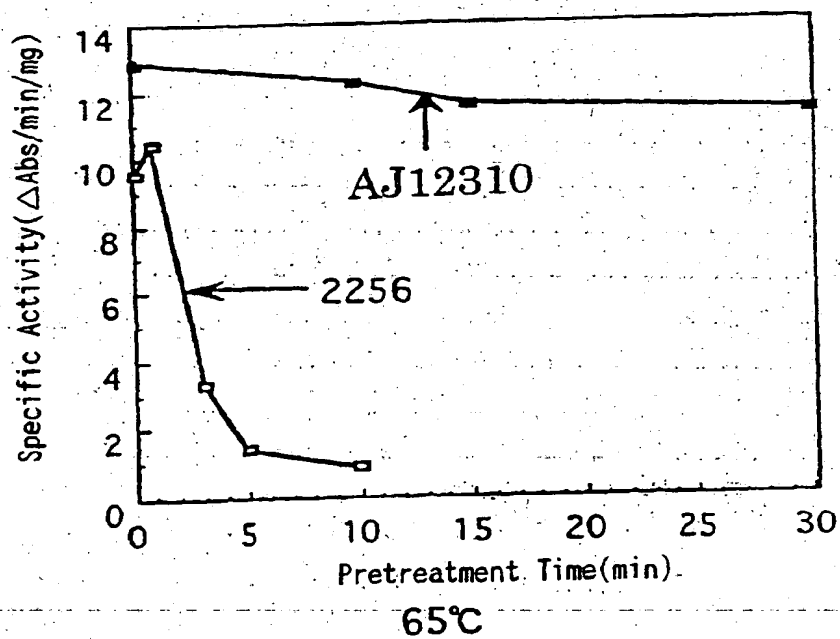


Fig. 2

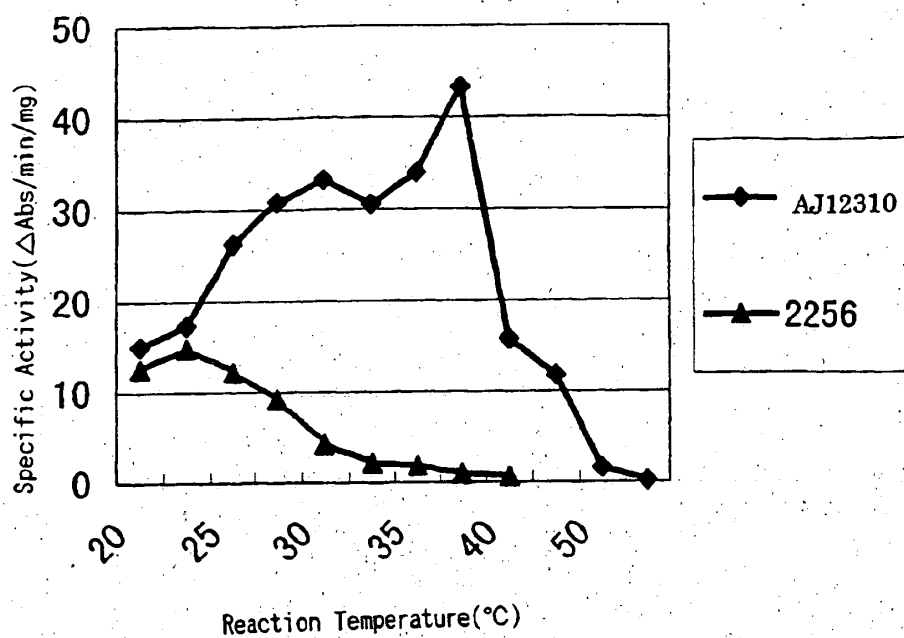


Fig. 3

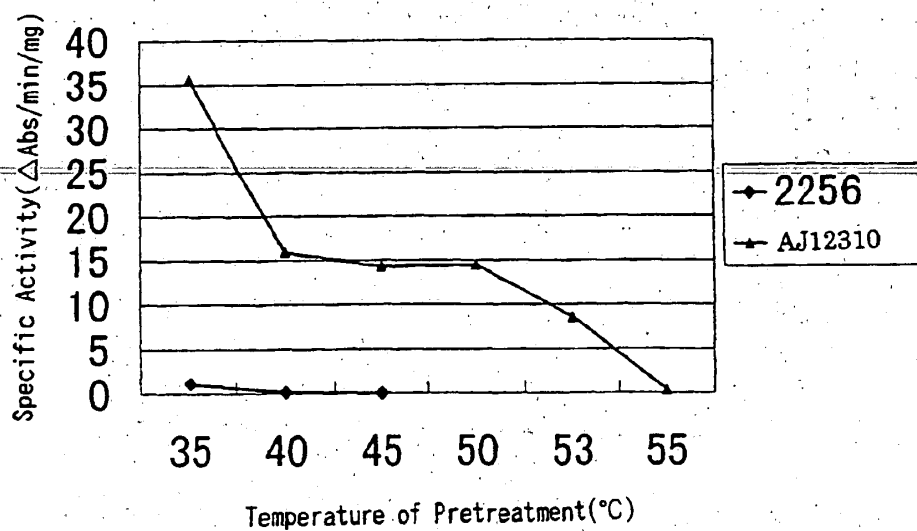


Fig. 4

Fig. 5

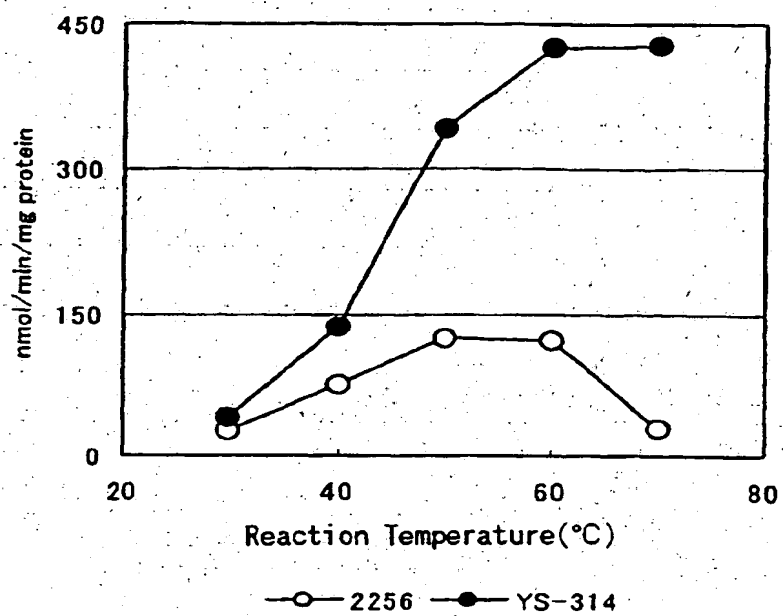


Fig. 6

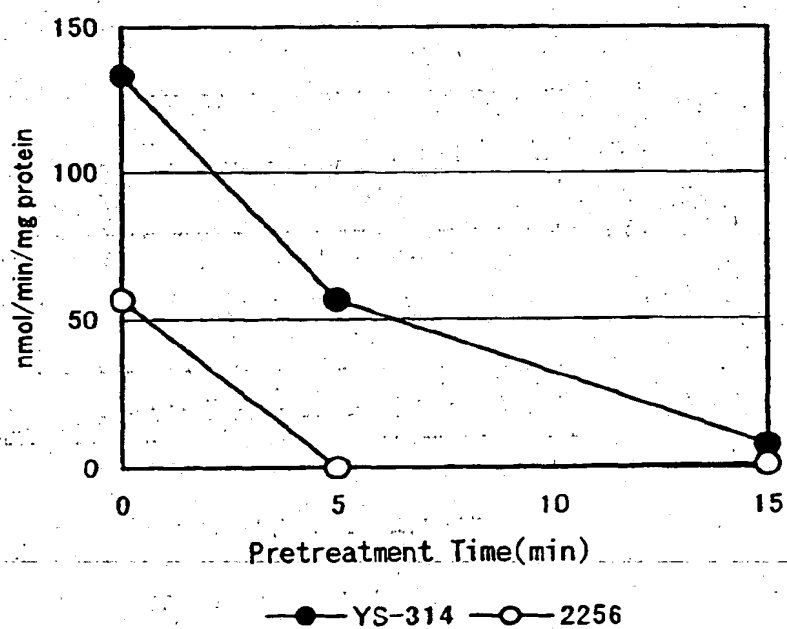


Fig. 7

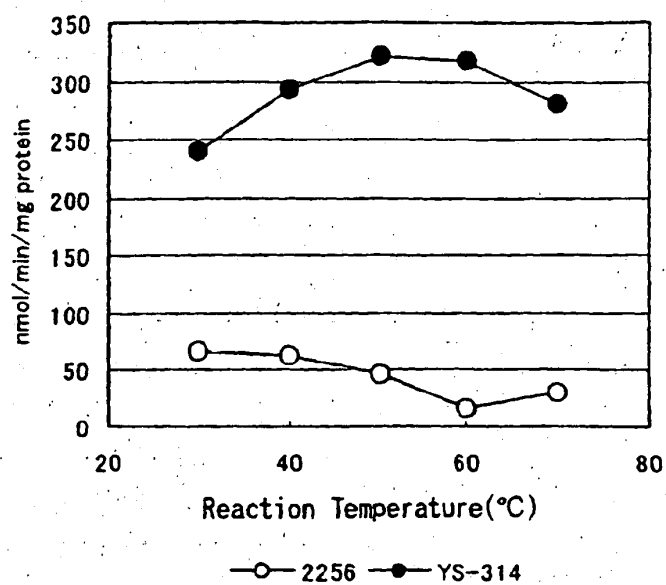


Fig. 8

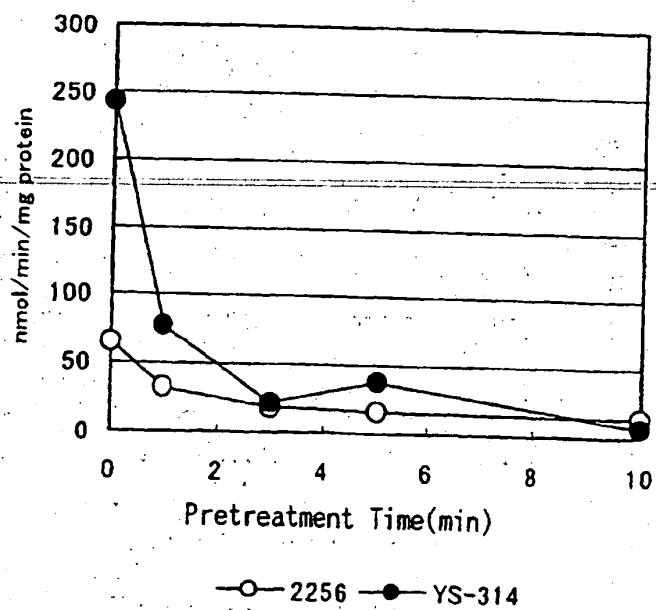


Fig. 9

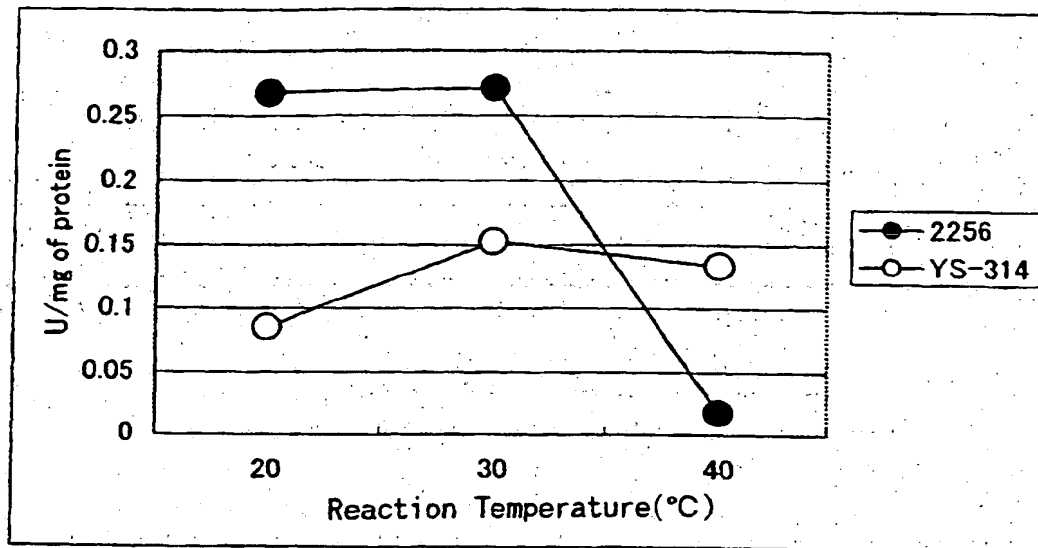


Fig. 10

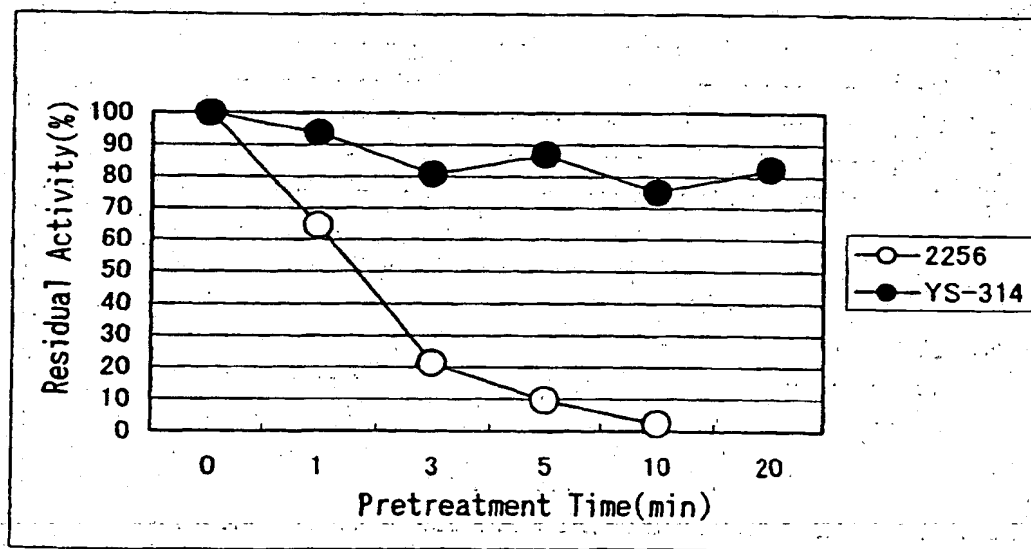


Fig. 11

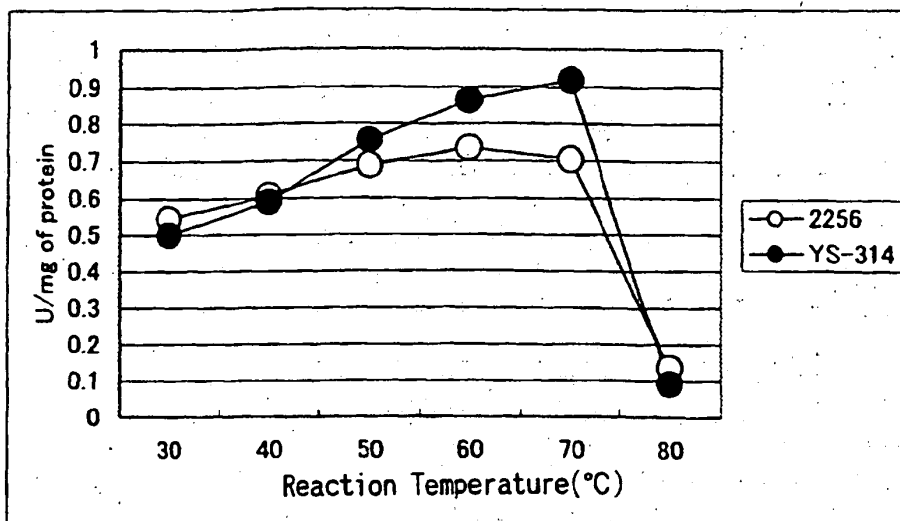


Fig. 12

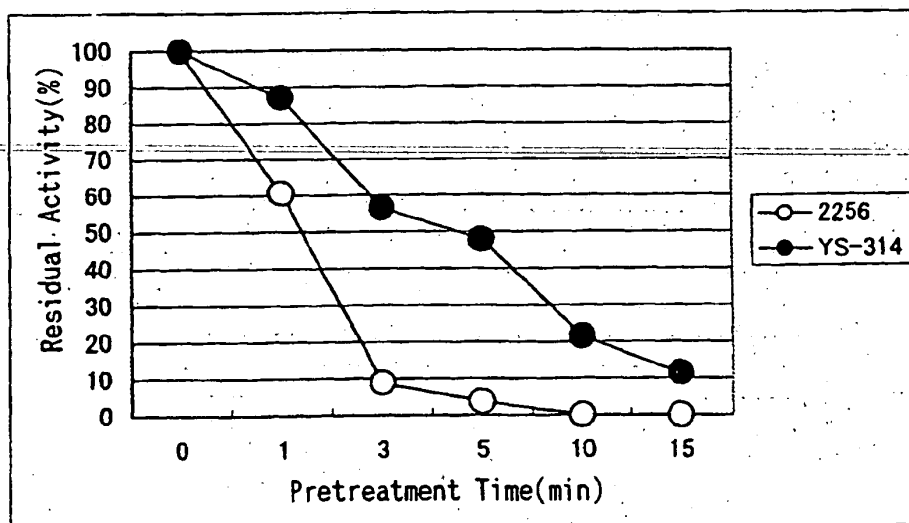


Fig. 13

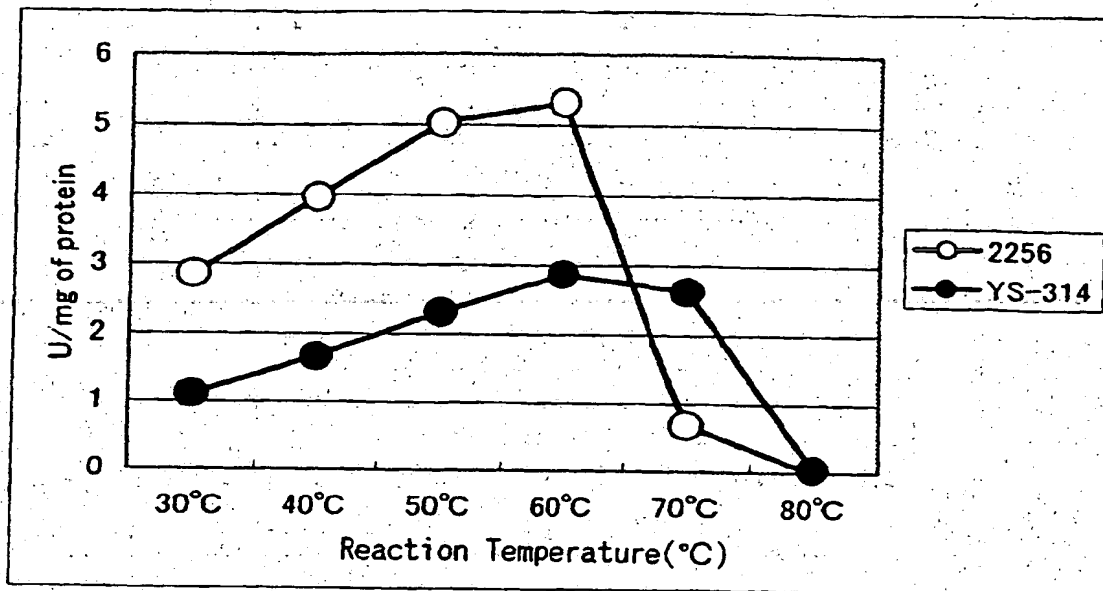
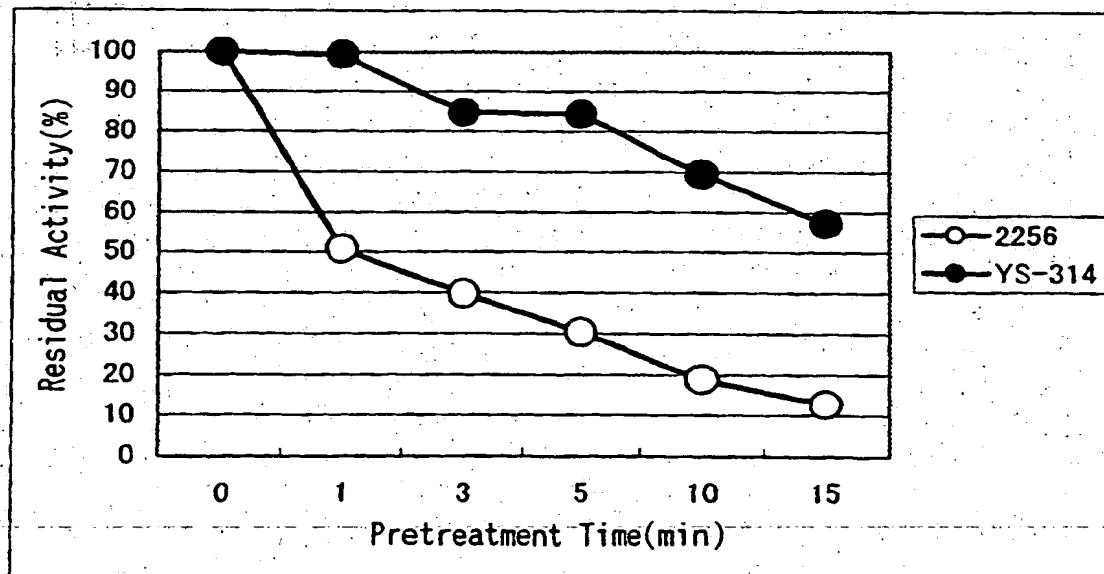
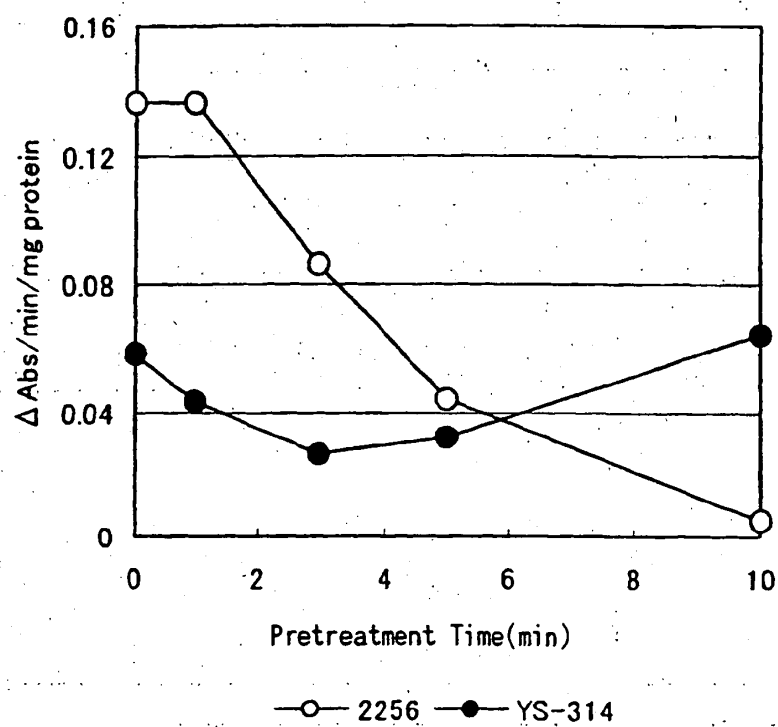


Fig. 14



*Fig. 15*

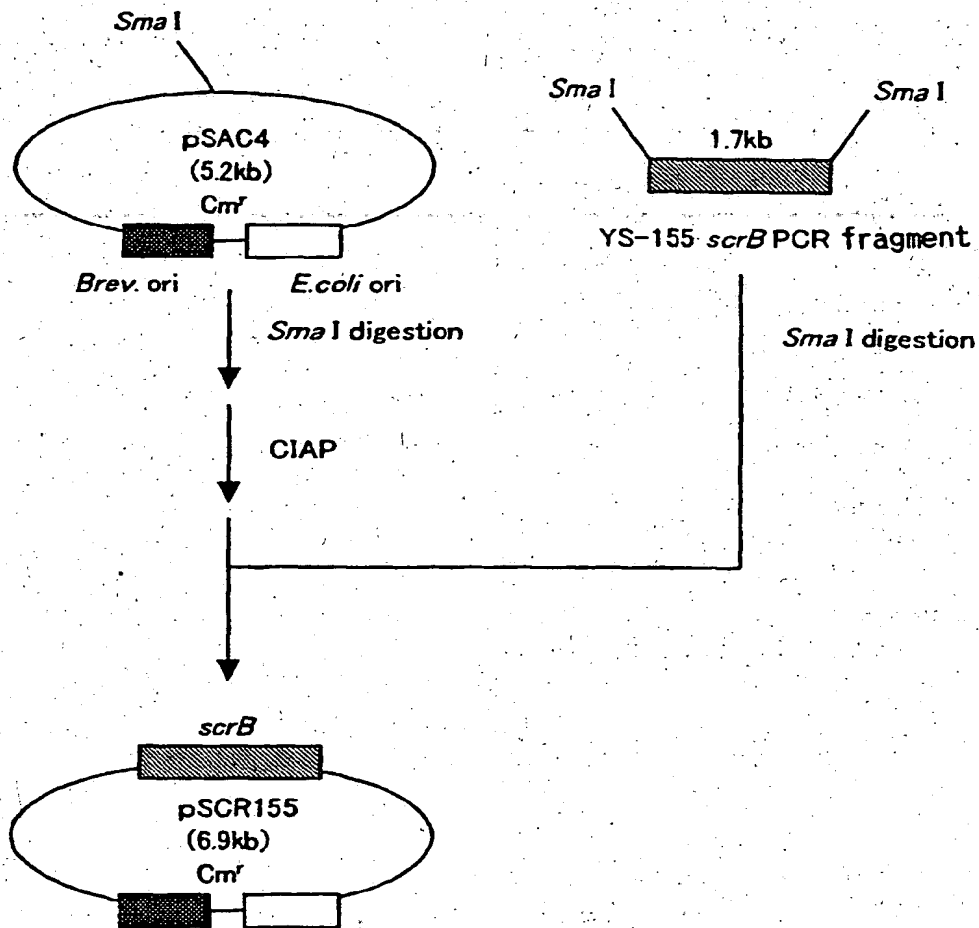


Fig. 16

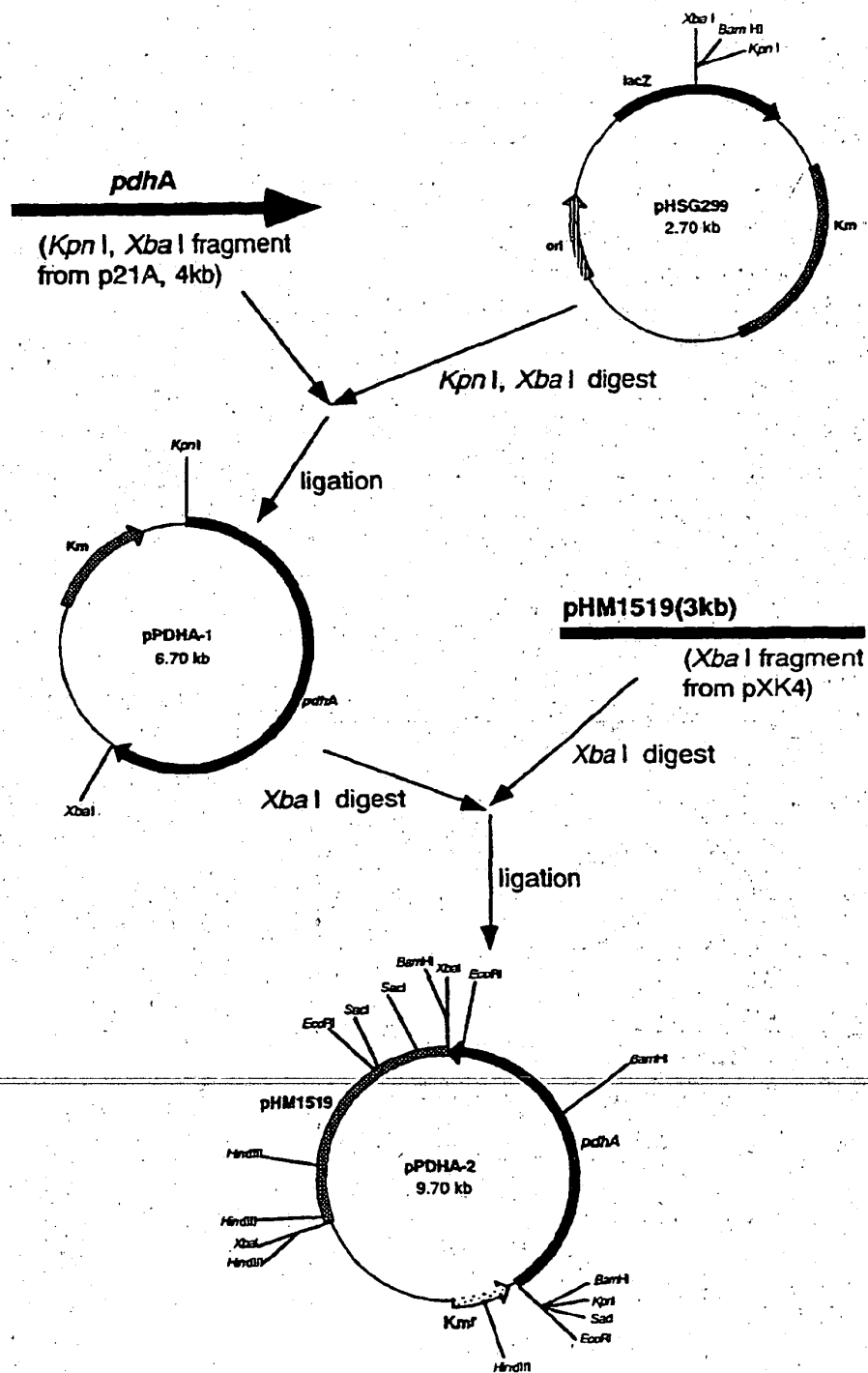


Fig. 17

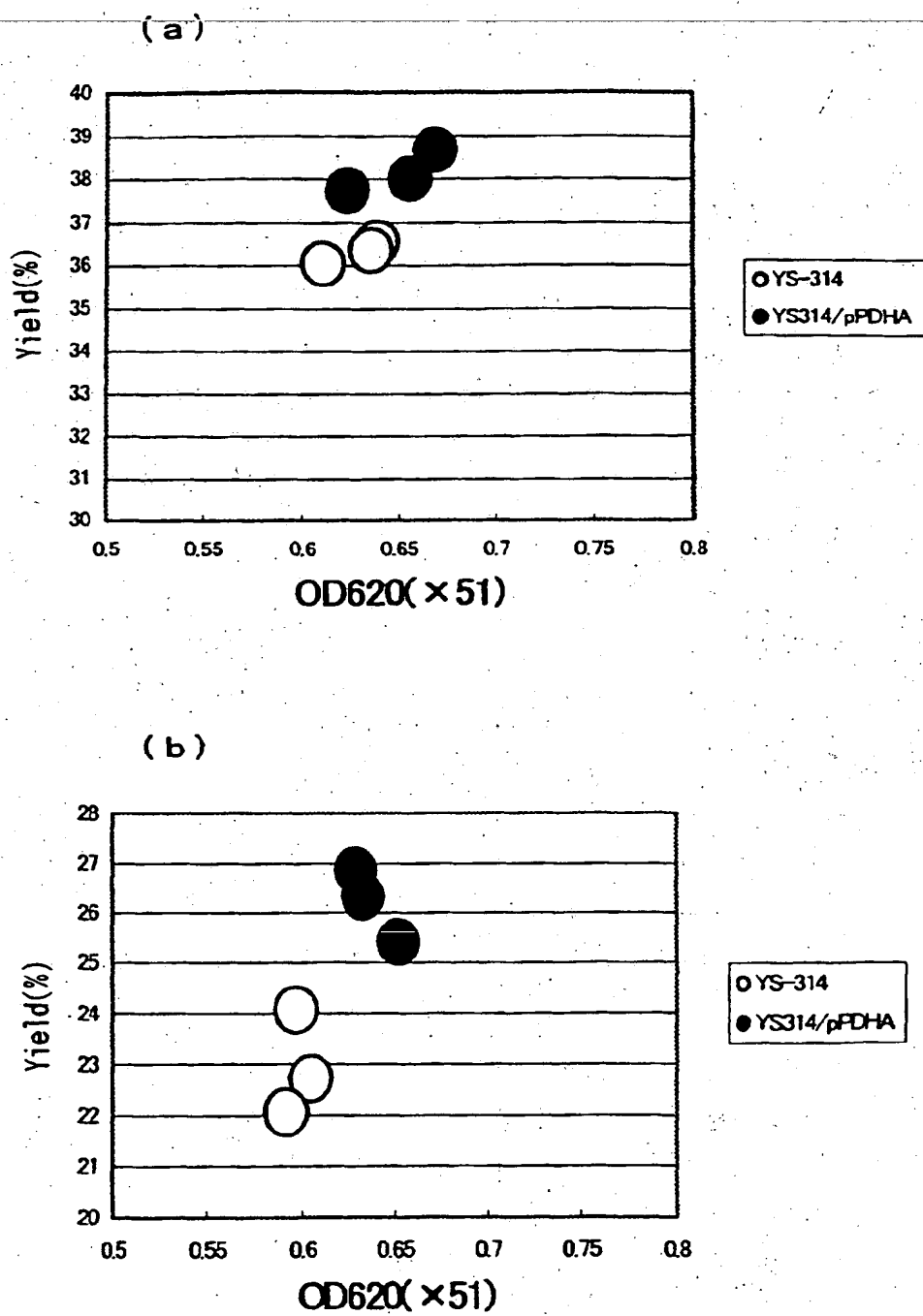


Fig. 18

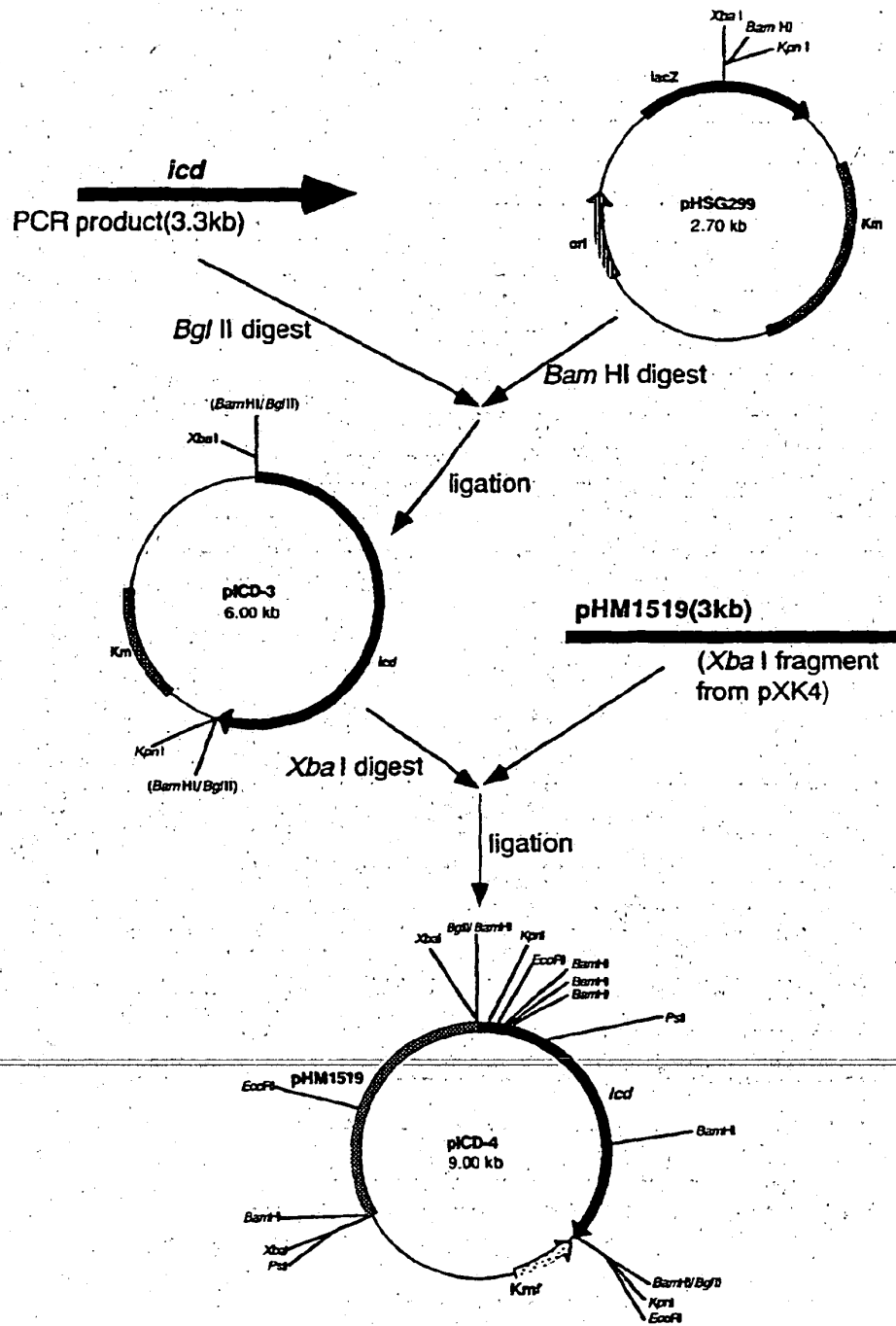


Fig. 19

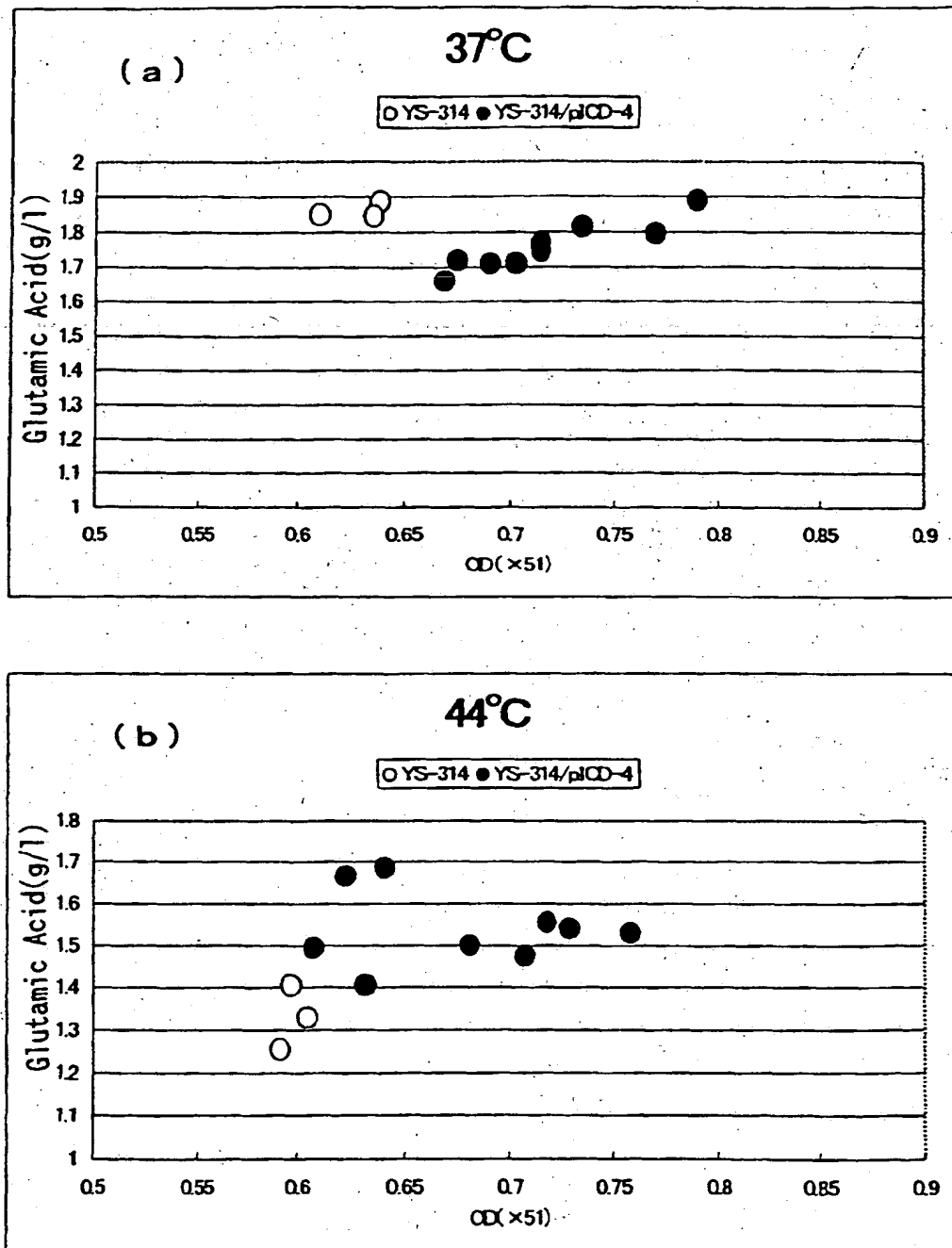


Fig. 20

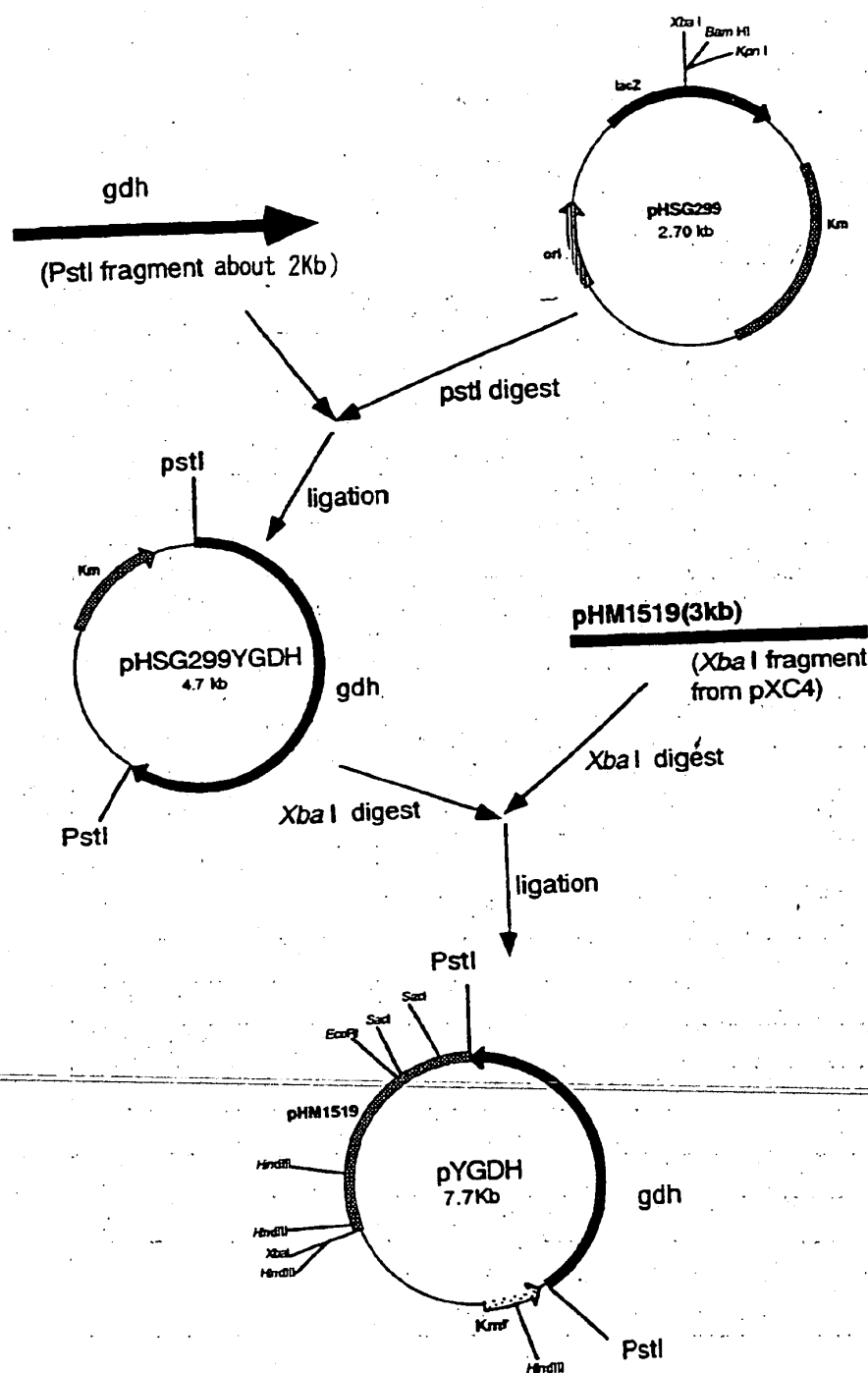


Fig. 21

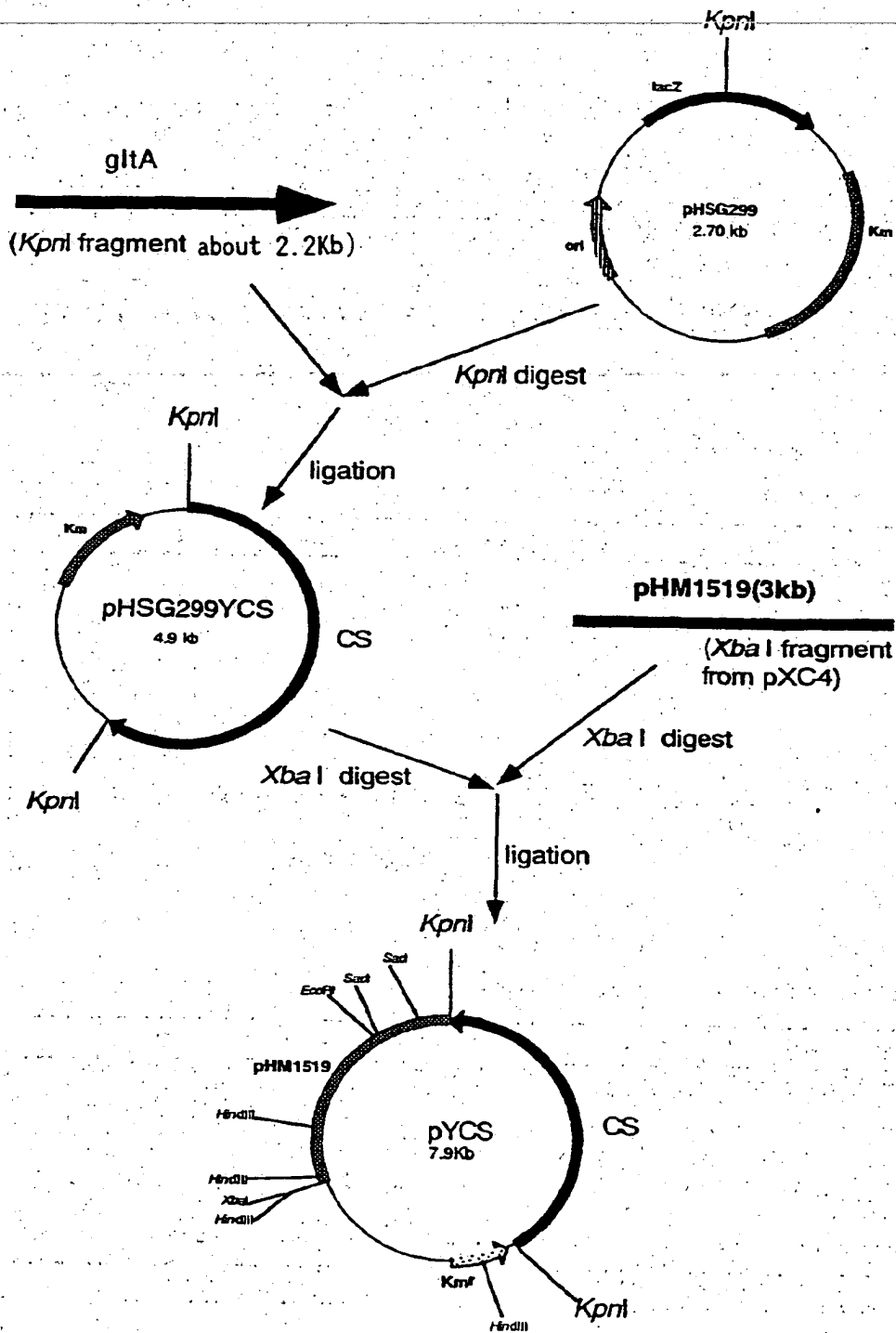


Fig. 22

INTERNATIONAL SEARCH REPORT

International application No.

PCT/JP00/06913

A. CLASSIFICATION OF SUBJECT MATTER

Int. Cl.⁷ C12N15/60, C12N15/54, C12N15/53, C12N15/31, C12N15/56, C12N9/88,
C12N9/12, C12N9/04, C07K14/34, C12N9/26, C12P13/04

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

Int. Cl.⁷ C12N15/60, C12N15/54, C12N15/53, C12N15/31, C12N15/56, C12N9/88,
C12N9/12, C12N9/04, C07K14/34, C12N9/26, C12P13/04

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
JICST FILE (JOIS), WPI (DIALOG), BIOSIS (DIALOG), MEDLINE (STN),
EMBL/DDBJ/Genbank/PIR/Swissprot/Geneseq

C. DOCUMENTS CONSIDERED TO BE RELEVANT

| Category* | Citation of document, with indication, where appropriate, of the relevant passages | Relevant to claim No. |
|-----------|---|-----------------------|
| Y | JP, 7-63383, B2, (Ajinomoto Co., Inc.), 12 July, 1995 (12.07.95), & FR, 2612937, A & US, 5250434, A & AU, 8811614, A & BR, 8801289, A & KR, 9606580, A | 1-49 |
| Y | JP, 4-4887, A (Ajinomoto Co., Inc.), 09 January, 1992 (09.01.92), & FR, 2661191, A & US, 5250423, A | 1-49 |
| Y | Microbiology, Vol.144 [5] (1998), K. Takai et al., "ppc, the gene for phosphoenolpyruvate carboxylase from an extremely thermophilic bacterium, Rhodothermus obamensis: Cloning, sequencing and overexpression in Escherichia coli", pp.1423-1434 | 1-49 |
| Y | JP, 5-56782, A (Ajinomoto Co., Inc.), 09 March, 1993 (09.03.93), & EP, 530765, A2 & US, 57700661, A & CA, 2077308, A & US, 5439822, A & TW, 260709, A & DE, 69217144, B | 1,17,18,49 |

☒ Further documents are listed in the continuation of Box C. ☐ See patent family annex.

* Special categories of cited documents:

"A" document defining the general state of the art which is not
considered to be of particular relevance

"E" earlier document but published on or after the international filing
date

"L" document which may throw doubts on priority claim(s) or which is
cited to establish the publication date of another citation or other
special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other
means

"P" document published prior to the international filing date but later
than the priority date claimed

"T" later document published after the international filing date or
priority date and not in conflict with the application but cited to
understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be
considered novel or cannot be considered to involve an inventive
step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be
considered to involve an inventive step when the document is
combined with one or more other such documents, such
combination being obvious to a person skilled in the art

"&" document member of the same patent family

Date of the actual completion of the international search
19 December, 2000 (19.12.00)

Date of mailing of the international search report
26 December, 2000 (26.12.00)

Name and mailing address of the ISA/
Japanese Patent Office

Authorized officer

Facsimile No.

Telephone No.

Form PCT/ISA/210 (second sheet) (July 1992)

INTERNATIONAL SEARCH REPORT

International application No.

PCT/JP00/06913

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT.

| Category* | Citation of document, with indication, where appropriate, of the relevant passages | Relevant to claim No. |
|-----------|--|-----------------------|
| Y | WO, 92/18635, A1 (Commonwealth Sci. & Ind. Res. Org.), 29 October, 1992 (29.10.92), & ZA, 9202761, A & AU, 9215771, A & NZ, 242370, A Fig. 5; Table 4 | 1, 17, 18, 49 |
| Y | Gene, Vol. 145 [1] (1994) D. Weweecke et al. "Cloning and sequence analysis of the gene encoding isocitrate lyase from <i>Rhodococcus fascians</i> " pp. 109-114 | 1, 17, 18, 19 |
| Y | Arch. Microbiol., Vol. 166 [2] (1996) W. Jager et al. "A <i>Corynebacterium glutamicum</i> gene encoding a two-domain protein similar to biotin carboxylases and biotin-carboxyl-carrier proteins" pp. 977-984 | 2, 19, 20, 49 |
| Y | Mol. Microbiol., Vol. 19 (1996) S. Donadio et al. "Erythromycin production in <i>Saccharopolyspora erythraea</i> does not require a functional propionyl-CoA carboxylase" pp. 977-984 | 2, 19, 20, 49 |
| Y | WO, 94/08016, A1 (Arch. Dev. Corp.), 14 April, 1994 (14.04.94), & EP, 663012, A1 & AU, 9352956, A & US, 5539092, A & US, 5756290, A & US, 5792627, A & US, 5972644, A Figs. 2, 3; sequence No. 6 | 2, 19, 20, 49 |
| Y | WO, 96/32484, A2 (Arch. Dev. Corp.), & EP, 820514, A1 & AU, 9655432, A & US, 5910626, A Claim 32; sequence No. 8 | 2, 19, 20, 49 |
| Y | Biosci. Biotechnol. Biochem., Vol. 60 (1996), E. Kimura et al., "Molecular cloning of a novel gene, <i>dtSR</i> , which rescues the detergent sensitivity of a mutant derived from <i>Brevibacterium lactofermentum</i> " pp. 1565-1570 | 3, 4, 21-24, 49 |
| Y | WO, 95/23224, A1 (Ajinomoto Co., Inc.), 31 August, 1995 (31.08.95), & EP, 752472, A1 & BR, 9506883, A & US, 5929221, A & DE, 69514914, B Claim 2, sequence No. 2 | 3, 4, 21-24, 49 |
| Y | JP, 10-234371, A (Ajinomoto Co., Inc.), 08 September, 1998 (08.09.98) (Family: none) | 3, 4, 21-24, 49 |
| Y | JP, 7-121227, B2 (KYOWA HAKKO KOGYO CO., LTD.), 25 December, 1995 (25.12.95) (Family: none) | 5, 25, 26, 49 |
| Y | J. Bacteriol., Vol. 178 (1996) A. M. Alves et al., "Characterization and phylogeny of the <i>pfp</i> gene of <i>Amycolatopsis methanolica</i> encoding PPI-dependent phosphofructokinase" pp. 149-155 | 5, 25, 26, 49 |
| Y | Appl. Environ. Microbiol., Vol. 63 (1997), A.M.C.R. Alves et al., "Identification of ATP-dependent phosphofructokinase as a regulatory step in the glycolytic pathway of the actinomycete <i>Streptomyces</i> <i>coelicolor</i> A3(2)" pp. 951-956 | 5, 25, 26, 49 |

Form PCT/ISA/210 (continuation of second sheet) (July 1992)

INTERNATIONAL SEARCH REPORT

International application No.

PCT/JP00/06913

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

| Category* | Citation of document, with indication, where appropriate, of the relevant passages | Relevant to claim No. |
|-----------|--|-----------------------|
| Y | J. Bacteriol., Vol.177(1995) W. Kronmeyer et al. "Structure of the <i>gluABCD</i> cluster encoding the glutamate uptake system of <i>Corynebacterium glutamicum</i> ", pp.1152-1158 | 7, 29, 30, 49 |
| Y | Eur. J. Biochem., Vol.227[1-2](1995), C. Rollin et al., "13C-NMR studies of <i>Corynebacterium melassecola</i> metabolic pathways" pp.488-493 | 8, 31, 32, 49 |
| Y | J. Bacteriol., Vol.176(1994), S. Hein et al., "Biochemical and molecular characterization of the <i>Alcaligenes eutrophus</i> pyruvate dehydrogenase complex and identification of new type of dihydrolipoamide dehydrogenase", pp.4394-4408 | 8, 31, 32, 49 |
| Y | Eur. J. Biochem., vol.133(1983), P. E. Stephens et al., "The pyruvate dehydrogenase complex of <i>Escherichia coli</i> K12. Nucleotide sequence encoding the pyruvate dehydrogenase component", pp.155-162 | 8, 31, 32, 49 |
| Y | WO, 99/18228, A2 (Forschungszentrum Juelich GmbH), 15 April, 1999 (15.04.99), & EP, 10125621, A2 & AU, 9911482, A & ZA, 9809014, A & DE, 19831609, A1 & SK, 200000481, A & BR, 9813021, A Claims 15, 18; sequence No. 2 | 9, 33, 34, 49 |
| Y | JP, 10-165180, A (Ajinomoto Co., Inc.), 23 June, 1998 (23.06.98), & EP, 857784, A2 & SK, 9701635, A & HU, 9702361, A2 & BR, 9706058, A | 10, 35, 36, 49 |
| Y | JP, 2-291276, A (Degussa AG.), 18 April, 1990 (18.04.90), & EP, 358940, A1 & GB, 2223754, A & DE, 68924227, B | 10, 35, 36, 49 |
| Y | JP, 11-196887, A (Mitsubishi Chemical Corporation), 27 July, 1999 (27.07.99) (Family: none) | 10, 35, 36, 49 |
| Y | JP, 8-66189, A (Mitsubishi Chemical Corporation), 12 March, 1996 (12.03.96) (Family: none) | 10, 35, 36, 49 |
| Y | MIKROBIOLOGIA, Vol.56[5](1987), M. P. Ruklish et al., "The functioning of the tricarboxylic acid cycle in <i>Brevibacterium flavum</i> and <i>Micrococcus glutamicus</i> ", pp.759-763 | 11, 37, 38, 49 |
| Y | J. Bacteriol., Vol.175(1993), J. M. Mengaud et al., "The major iron-containing protein of <i>Legionella pneumophila</i> is an aconitase homologous with the human iron-responsive element-binding protein" pp.5666-5676 | 11, 37, 38, 49 |
| Y | Eur. J. Biochem. Vol.204(1992), c. Prodromou et al., "The aconitase of <i>Escherichia coli</i> . Nucleotide sequence of the aconitase gene and amino acid sequence similarity with mitochondrial isopropylmalate isomerases", pp.599-609 | 11, 37, 38, 49 |

Form PCT/ISA/210 (continuation of second sheet) (July 1992)

INTERNATIONAL SEARCH REPORT

International application No.

PCT/JP00/06913

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

| Category* | Citation of document, with indication, where appropriate, of the relevant passages | Relevant to claim No. |
|-----------|---|-----------------------|
| Y | J. Bacteriol., Vol.177(1995), B. J. Eikmanns et al., "Cloning, sequence analysis, expression, and inactivation of the <i>Corynebacterium glutamicum</i> <i>icd</i> gene encoding isocitrate dehydrogenase and biochemical characterization of the enzyme", pp.774-782 | 12,39,40,49 |
| Y | J. Bacteriol., Vol.175(1993), A. Ishi et al., "Genes encoding two isocitrate dehydrogenase isozymes of a psychrophilic bacterium, <i>Vibrio</i> sp. Strain ABE-1", pp.6873-6880 | 12,39,40,49 |
| Y | Genbank, Acc. No. Y16642 (01 February, 1999), B. J. Eikmanns et al., "Corynebacterium glutamicum <i>lpd</i> gene, complete CDS" | 13,41,42,49 |
| Y | WO, 97/48790, A1 (Ajinomoto Co., Inc.), 24 December, 1997 (24.12.97), & JP, 10-87, A & EP, 974647, A1 Claims; pages 38-40; sequence No. 7 | 14,43,44,49 |
| Y | WO, 95/34672, A1 (Ajinomoto Co., Inc.), 21 December, 1995 (21.12.95), & US, 5977331, A & EP, 771879, A1 Claims; sequence Nos. 1, 2 | 14,43,44,49 |
| Y | Mol. Microbiol., Vol.,6(1992), E. R. Boermann et al., "Molecular analysis of the <i>Corynebacterium glutamicum</i> <i>gdh</i> gene encoding glutamate dehydrogenase", pp.317-326 | 15,45,46,49 |
| Y | JP, 6-502548, A (Orsan), 24 March, 1994 (24.03.94), & EP, 551506, A1 & WO, 93/03158, A1 & FR, 2679921, A1 & FR, 2679922, A1 & US, 6027920, A | 15,45,46,49 |
| Y | Microbiology, Vol.140(1994), B. J. Eikmanns et al., "Nucleotide sequence, expression and transcriptional analysis of the <i>Corynebacterium glutamicum</i> <i>gltA</i> gene encoding citrate synthase", pp.1817-1828 | 16,47,48,49 |
| Y | Mol. Microbil., Vol.11(1994), M. A. Pardo et al., "Nodulation ability of <i>Rhizobium tropici</i> is conditioned by a plasmid-encoded citrate synthase", pp.315-321 | 16,47,48,49 |
| Y | JP, 8-196280, A (Ajinomoto Co., Inc.), 06 August, 1996 (06.08.96), & EP, 724017, A2 & FR, 2729970, A & SK, 9600112, A & ZA, 9600656, A & BR, 9600268, A | 6,27,28,49 |
| Y | JP, 5-244958, A (Ajinomoto Co., Ltd.), 24 September, 1993 (24.09.93), & US, 5556776, A | 6,27,28,49 |

Form PCT/ISA/210 (continuation of second sheet) (July 1992)